```
                GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:        September 10, 2005, 22:15:12.; Search time 5992.54 Seconds
                                             (without alignments)
                               10576.393 Million cell updates/sec

Title:          US-10-632-436A-1
Perfect score:  1308
Sequence:       1 gtacacatataccaacata.......ttaaaaagggtacttagat 1308

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters:       9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
          1: gb_ba:*
          2: gb_htg:*
          3: gb_in:*
          4: gb_om:*
          5: gb_ov:*
          6: gb_pat:*
          7: gb_ph:*
          8: gb_pl:*
          9: gb_pr:*
         10: gb_ro:*
         11: gb_sts:*
         12: gb_sy:*
         13: gb_un:*
         14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	1308	100.0	103157	8	AC011810	Arabidops
	2	1295.8	99.1	1312	8	AY063855	Arabidops
	3	1264	96.6	1276	8	AB013886	Arabidops
	4	1255	95.9	1281	6	AR439833	Sequence
	5	1066	81.5	1066	8	AY091291	Arabidops
	6	1035	79.1	1035	6	AX507621	Sequence
	7	517.8	39.6	1002	8	ATH441073	Arabidops
	8	517.8	39.6	1242	8	AY087951	Arabidops
	9	517.8	39.6	77483	8	AB028607	Arabidops
	10	393.2	30.1	1279	8	AY056169	Arabidops
	11	391.2	29.9	1376	8	AY091069	Arabidops
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	13	389.8	29.8	1117	8	AY122941	Arabidops
c	14	379.4	29.0	96808	8	AC011914	Arabidops
	15	379.4	29.0	100515	8	AC011665	Arabidops
	16	378.4	28.9	1311	8	AY085908	Arabidops
	17	378.4	28.9	1315	8	AB013887	Arabidops
	18	378.4	28.9	1330	8	AF360312	Arabidops
	19	374.6	28.6	1113	8	AF003101	Arabidops
	20	369.8	28.3	1090	8	AY056361	Arabidops
	21	368	28.1	1059	6	AX507121	Sequence
	22	368	28.1	1059	6	AX651568	Sequence
c	23	212.6	16.3	170226	8	AP003450	Oryza sat
	24	209.2	16.0	1470	8	BT009310	Triticum
	25	190.4	14.6	1098	6	AX660402	Sequence
	26	189.8	14.5	1098	6	AX654175	Sequence
	27	189.8	14.5	1098	8	AK660052	Arabidops
	28	189.8	14.5	1512	8	AK065008	Oryza sat
	29	189.8	14.5	141862	8	AP002913	Oryza sat
	30	183.2	14.0	930	6	AX654438	Oryza sat
	31	178.2	13.6	141715	8	AC130725	Oryza sat
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	33	178.2	13.6	177861	8	AC135925	Oryza sat
	34	152.4	11.7	274	11	AL823960	Arabidops
	35	140	10.7	1126	8	AY085197	Arabidops
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	37	140	10.7	142001	8	AL138642 / ATF21F14	Arabidops
	38	132.2	10.1	477	6	AX505488	Sequence
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	40	132.2	10.1	994	8	AK117587	Arabidops
c	41	132.2	10.1	31733	8	AC007135	Arabidops
	42	132.2	10.1	120938	8	AC007017	Arabidops
	43	132	10.1	933	6	AX589947	Sequence
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ALIGNMENTS

```
RESULT 1
AC011810
LOCUS       AC011810        103157 bp    DNA     linear   PLN 01-SEP-2000
DEFINITION  Arabidopsis thaliana chromosome I BAC T6J4 genomic sequence,
            complete sequence.
ACCESSION   AC011810
VERSION     AC011810.8  GI:8576186
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 103157)
AUTHORS     Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S.,
            Buehler,E., Chao,Q., Chin,C., Chiou,J., Choi,E., Gonzalez,A.,
            Howng,B., Johnson-Hopson,C., Khan,S., Kim,C., Koo,T., Lee,J.M.,
            Lenz,C., Liu,A., Liu,S., Mukharsky,N., Pham,P., Sakano,H.,
            Shinn,P., Toriumi,M., Vaysberg,M., Yu,G., Ecker,J., Theologis,A.
            and Davis,R.W.
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 103157)
AUTHORS     Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E.,
            Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,
            Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,
            Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,
            Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,
            Theologis,A. and Davis,R.W.
TITLE       Direct Submission
JOURNAL     Submitted (15-OCT-1999) DNA Sequencing and Technology Center,
            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
REFERENCE   3 (bases 1 to 103157)
AUTHORS     Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
            Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buehler,E.,
            Chin,C., Chiou,J., Choi,E., Dunn,P., Gonzalez,A., Howng,B., Kim,C.,
            Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S.,
            Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P.,
            Thaveri,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J.,
            Theologis,A. and Davis,R.W.
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TITLE   Direct Submission
JOURNAL   Submitted (01-JUN-2000) DNA Sequencing and Technology Center,
          Stanford University, 855 California Avenue, Palo Alto, CA 94304,
          USA
REFERENCE 4 (bases 1 to 103157)
AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
          Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
          and Davis,R.W.
TITLE   Direct Submission
JOURNAL   Submitted (21-JUN-2000) DNA Sequencing and Technology Center,
          Stanford University, 855 California Avenue, Palo Alto, CA 94304,
          USA
REFERENCE 5 (bases 1 to 103157)
AUTHORS   Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F.,
          Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A.
          and Davis,R.W.
TITLE   Direct Submission
JOURNAL   Submitted (01-SEP-2000) DNA Sequencing and Technology Center,
          Stanford University, 855 California Avenue, Palo Alto, CA 94304,
          USA
COMMENT   On Jun 21, 2000 this sequence version replaced gi:8050909.
          Bases 1-5,179 of clone T6J4 overlap with bases 94,580-99,758 of IGF
          BAC clone F3F19 (gb|AC007357).
          e-mail for correspondence: arab@sequence.stanford.edu Genes with
          similarity to proteins in the databases are named 'putative',
          '-like', or 'similar to'. Genes that have EST similarity but no
          significant protein similarity are described as 'unknown proteins'.
          Genes that are annotated based only on gene prediction software
          are described as 'hypothetical proteins'. The gene prediction
          programs used to predict genes include: Grail (Informatics Group,
          Oak Ridge National Laboratory,
          http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,
          http://genes.mit.edu/GENSCAN.), FEXA (Victor Solovyev,
          http://genomic.sanger.ac.uk/gf/gf.shtml), and NetPlantGene (S.M.
          Hebsgaard, et al., http://www.cbs.dtu.dk/NetPlantGene.html).
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     misc_feature 1..5179
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Query Match   100.0%;   Score 1308; DB 8; Length 103157;
Best Local Similarity   100.0%;   Pred. No. 5.8e-277;
Matches 1308; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 GTTTTCAAACCATAAAAAAAAAAACACAGATTAAATGGAATCGAGTAGCGTTGATGAGAGTAC 120
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Qy   121 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTTCCGGCGAAAAAGTCGTCGGT 180
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Qy   181 AGGTAACTTATACAGGATGGGAAGCGGATCAAGCGGTTGTGTTAGATTCAGAGAACGGCGT 240
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Db   20585 AGGTAACTTATACAGGATGGGAAGCGGATCAAGCGGTTGTGTTAGATTCAGAGAACGGCGT 20644

Qy   241 AGAAGCTGAATCTAGGAGAGCTTCCGTCGTCTCGTCAAAATACAAAGGTGGTGCCACAACCAAA 300
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Qy   301 CGGAGAGATGGGGAGCTCAGATTTACGAGAAACACCAGCGCGTGCGTGGCTCGGACATTCAA 360
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Qy   481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAAACGAAGAGTTAGA 540
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Qy   541 GCAGAGTAAACGGCGTCGTAATGGTAACGGAAACAATGACTAGGACGTTGTTAACCTCGGG 600
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Qy   601 GTTGAGTAATGATGGTGTTTCTACGACGGGGTTAGATCGGCCGGAGGCACTGTTCGAGAA 660
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Qy   841 TTATGTTTGACTAAAGGTTGGACAGGTTCGTTCGTTAAGGAGAAGAATCTACGTGCTGGTGA 900
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Qy   901 CGTGGTTAGTTCAGTAGATCTAACGGTCAGGATCAACACAGTTGTACATTGGTGGAAGTC 960
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Qy   1021 ACCGGAGAGTTCAAGAAACCAGACGTCGTAGGAAACAAAGAGTGAACGATACTGAGATGTT 1080
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Qy   1141 TTTTTTTCTTTGTTGTTTAATAATTTTTAAAAACTCCATTTCGTTTTCTTTATTTG 1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1201 CATCGGTTTCTTTCTTCTTCGTTGTTACCAAAGGTTCATGAGTTGTTTTTGTTGTATTGATGA 1260
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RESULT 2
AY063855
LOCUS   AY063855   1312 bp   mRNA   linear   PLN 18-SEP-2002
DEFINITION   Arabidopsis thaliana putative DNA-binding protein RAV1 (At1g13260)
                mRNA, complete cds.
ACCESSION   AY063855
VERSION   AY063855.1   GI:17380761
KEYWORDS   FLI cDNA.
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM   Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 1312)
  AUTHORS   Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
                Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
                Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
                Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
                Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
                Satou,M., Seki,M., Shinn,P., Southwick,A.M.,
                Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE   Arabidopsis Full Length cDNA Clones
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1312)
  AUTHORS   Yamada,K., Banh,J., Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D.,
                Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C.,
                Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H.,
                Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A.,
                Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J.,
                Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
                Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
                Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE   Direct Submission
  JOURNAL   Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan
                Street, Albany, CA 94710, USA
COMMENT   RIKEN Genomic Sciences Center (GSC) members carried out the RIKEN
                collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
                Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,

Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J.,
Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C.,
Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T.,
Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C.,
Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki.M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.

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                     /note="This clone is in a modified pBluescript vector
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ORIGIN

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Best Local Similarity  99.8%;   Pred. No. 2.1e-274;
Matches 1297;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;
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Qy   969 GGTCAGATTTAGATGCGGGTCGGGTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGA 1028
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RESULT 3
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LOCUS       AB013886              1276 bp    mRNA    linear   PLN 06-FEB-1999
DEFINITION  Arabidopsis thaliana mRNA for RAV1, complete cds.
ACCESSION   AB013886
VERSION     AB013886.1  GI:3868856
KEYWORDS    RAV1.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (sites)
  AUTHORS   Kagaya,Y., Ohmiya,K. and Hattori,T.
  TITLE     RAV1, a novel DNA-binding protein, binds to bipartite recognition
            sequence through two distinct DNA-binding domains uniquely found in
            higher plants
  JOURNAL   Nucleic Acids Res. 27 (2), 470-478 (1999)
  MEDLINE   99081843
   PUBMED   9862967
REFERENCE   2  (bases 1 to 1276)
  AUTHORS   Hattori,T. and Kagaya,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-1998) Tsukaho Hattori, Mie University, Center for
            Molecular Bilogy and Genetics; 1515 Kamihama-cho, Tsu, Mie
            514-8507, Japan (E-mail:hattori@gene.recs.mie-u.ac.jp,
            Tel:81-592-231-9074, Fax:81-592-231-9048)
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match      96.6%;  Score 1264;  DB 8;  Length 1276;
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Matches 1275;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;
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Qy   214 CGTTGTGTTAGATTCAGAGAACGGGCTAGAAGCTTAGGAGCTTCCGTCGTCAAA 273
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Qy   334 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGACGAGAGCCGCTCGTCGTCCTACGAGCGT 393
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Qy   394 CGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAGATGGA 453
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Qy   694 CCGTTTGGTTATACCGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTTCAAGTAACGT 753
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Qy  1233 TCATGAGTTGTTTTTGTGTATTGATGAACTGTAAATTTTATTATAGGATAAATTTTAA 1292
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RESULT 4
AR439833
LOCUS       AR439833              1281 bp    DNA     linear   PAT 20-FEB-2004
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Qy  1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1108
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Db  1200 AGGTTCATGAGTTGTTTTTGTTGTTATTGATGAACTGTAAATTTATTTATTATAGGATAATT 1259

Qy  1289 TTAAAAA 1295
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Db  1260 TTAAAAA 1266
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RESULT 5
AY091291

LOCUS       AY091291    1066 bp    mRNA    linear    PLN 18-SEP-2002
DEFINITION  Arabidopsis thaliana putative DNA-binding protein RAV1 (At1g13260)
            mRNA, complete cds.
ACCESSION   AY091291
VERSION     AY091291.1  GI:20259028
KEYWORDS    FLI_CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1066)
AUTHORS     Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
            Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
            Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
            Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
            Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
            Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
            Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE       Arabidopsis Open Reading Frame (ORF) Clones
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 1066)
AUTHORS     Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
            Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
            Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
            Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
            Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
            Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
            Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
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DEFINITION  Sequence 65 from patent US 6664446.
ACCESSION   AR439833
VERSION     AR439833.1  GI:42665798
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1281)
AUTHORS     Heard,J., Broun,P., Riechmann,J.L., Keddie,J., Pineda,O., Adam,L.,
            Samaha,R., Zhang,J.-Y., Yu,G.-L., Ratcliffe,O., Pilgrim,M.,
            Jiang,C.-Z. and Reuber,L.
TITLE       Transgenic plants comprising polynucleotides encoding transcription
            factors that confer disease tolerance
JOURNAL     Patent: US 6664446-A 65 16-DEC-2003;
FEATURES             Location/Qualifiers
     source          1..1281
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match  95.9%;  Score 1255;  DB 6;  Length 1281;
Best Local Similarity  99.9%;  Pred. No. 2e-265;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;
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Qy   29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAACACAGAT 88
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120

Qy  149 CCGGCGATAACTCCGGCGAAAAGTCGTCGTAGTAGTAACTTATACAGGATGGGAAGCGGA 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 CCGGCGATAACTCCGGCGAAAAGTCGTCGTAGTAGTAACTTATACAGGATGGGAAGCGGA 180

Qy  209 TCAAGCGTTGTGTTAGATTCAGAGAACCGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TCAAGCGTTGTGTTAGATTCAGAGAACCGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy  269 TCAAAATACAAAAGGTGTGGTGCCACAACCAACCGGAGATGGGGAGCTCAGATTTACGAG 328
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 TCAAAATACAAAAGGTGTGGTGCCACAACCAAACCGGAGATGGGGAGCTCAGATTTACGAG 300

Qy  329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy  389 GACGTCGCGGTTCACAGGTTCCGTCCGTCGACGGCCGTCACAAATTTCAAAGACGTGAAG 448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GACGTCGCGGTTCACAGGTTCCGTCCGTCGACGGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy  449 ATGGACGAAGACGAGGTCGATTCTTCATTCGAATTCTTCATTCGAATCTCGAGATCGTTGATATG 508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 ATGAGACGAAGACGAGGTCGATTCTTCATTCGAATTCTTCATTCGAATCTCGAGATCGTTGATATG 480

Qy  509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTTAGAGCAGCGTCGTAATGGTAAC 568
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTTAGAGCAGCGCTCGTAATGGTAAC 540

Qy  569 GGAAACATGACTAGGACGGTTGTTAACGTCGGGGTTGTTAACGTCGGGGTTGTTTCTACGACG 628
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GGAAACATGACTAGGACGGTTGTTAACGTCGGGGTTGTTAACGTCGGGGTTGTTTCTACGACG 600

Qy  629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTTAACGCCAAGCGACGTTGGGAAG 688
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTTAACGCCAAGCGACGTTGGGAAG 660

Qy  689 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy  749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
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332  CACCAGCCGCTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGAC  391
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241  CACCAGCCGCTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGAC  300

392  GTCCGGTTCACAGGTTCCGTCGCCGTGCGCCGCCCTCACAAATTCAAAGACGTGAAGATG  451
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301  GTCGCGGTTCACAGGTTCCGTCGCCGTGCGCCGCGCCTCACAAATTCAAAGACGTGAAGATG  360

452  GACGAAGAGCAGAGGTCGATTTCTGAATTCATTCGAAATCTGAGATCGTTGATATGTTG  511
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361  GACGAAGAGCAGAGGTCGATTTCTGAATTCATTCGAAATCTGAGATCGTTGATATGTTG  420

512  AGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGA  571
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421  AGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGA  480

572  AACATGACTAGGAGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTTTCTACGACGGGG  631
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481  AACATGACTAGGAGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTTTCTACGACGGGG  540

632  TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCGTTGGGAAGCTA  691
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
541  TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCGTTGGGAAGCTA  600

692  AACCGTTGTTATACCGAGAACATCAGCAGAGAAACATTTTCCGTTACCGTCAAGTAAC  751
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601  AACCGTTTGTTATACCGAGAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAAC  660

752  GTTTCCGTGAAAGGAGTGTTGTTGAACTTGAACGGAAAGTGTGGAGGTTC  811
     ||||||||||||||||||||||||||||||||||||||||||||||||||
661  GTTTCCGTGAAAGGAGTGTTGTTGAACTTGAACGGAAAGTGTGGAGGTTC  720

812  CGTTACTCGTATTGAAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTTC  871
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
721  CGTTACTCGTATTGAAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTTC  780

872  GTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAG  931
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
781  GTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAG  840

932  GATCAACAGTTGTACATTGGGTGGAAGTCCGGGTCAGATTTAGATGCGGGTCGG  991
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
841  GATCAACAGTTGTACATTGGGTGGAAGTCCGGGTCAGATTTAGATGCGGGTCGG  900

992  GTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTAGGA  1051
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901  GTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTAGGA  960

1052 AACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGGAACGCATC  1111
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961  AACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGGAACGCATC  1020

1112 TTTCACGCCTGTAACAACTCTTCTTCTTTCTTTTTTTTGTTG  1157
     ||||||||||||||||||||||||||||||||||||| |||||
1021 TTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTTCTTTTGTTG  1066


RESULT 6
AX507621
LOCUS        AX507621              1035 bp    DNA        linear   PAT 27-SEP-2002
DEFINITION   Sequence 2316 from Patent WO0216655.
ACCESSION    AX507621
VERSION      AX507621.1  GI:23388858
KEYWORDS     .
SOURCE       Arabidopsis thaliana (thale cress)
  ORGANISM   Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE    1
  AUTHORS    Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
  TITLE      Stress-regulated genes of plants, transgenic plants containing
             same, and methods of use
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Qy  92  ATGGAATCAGTAGCGTTGATGAGAGTACTACAAGTACACAGTTCCATCGTGAAACCCG  151
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Db   1  ATGGAATCAGTAGCGTTGATGAGAGTACTACAAGTACACAGTTCCATCGTGAAACCCG  60

Qy 152  GCGATAACTTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA  211
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  GCGATAACTTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA  120

Qy 212  AGCGGTTGTGTTAGATTCAGAGAACGACGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCA  271
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  AGCGGTTGTGTTAGATTCAGAGAACGACGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCA  180

Qy 272  AAATACAAAGGTGTGTGCCACCAACCAAACGGAAGATGGGGAGCTCAGATTTACGAGAAA  331
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181  AAATACAAAGGTGTGTGCCACCAACCAAACGGAAGATGGGGAGCTCAGATTTACGAGAAA  240
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JOURNAL      Patent: WO 0216655-A 2316 28-FEB-2002;
             The Scripps Research Institute (US) ; Syngenta Participations AG
             (CH)
FEATURES             Location/Qualifiers
     source          1..1035
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
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ORIGIN

Query Match       79.1%;  Score 1035;  DB 6;  Length 1035;
Best Local Similarity   100.0%;  Pred. No. 4.7e-217;
Matches 1035;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;

Qy      92  ATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCG  151
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Db       1  ATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCG   60

Qy     152  GCGATAACTCCGCGCCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA  211
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  GCGATAACTCCGCGCCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA  120

Qy     212  AGCCGTTGTGTTAGATTCAGAGAACGGCGTAGAACGGCGTAGGAGAGCTTCCGTCGTCA  271
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  AGCCGTTGTGTTAGATTCAGAGAACGGCGTAGAACGGCGTAGGAGAGCTTCCGTCGTCA  180

Qy     272  AAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAGAAA  331
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  AAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAGAAA  240

Qy     332  CACCAGCGCGTGTGGCTCGGGACATTCAACGAGAAGACGAAGCCGCTCGTGCCTACGAC  391
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  CACCAGCGCGTGTGGCTCGGGACATTCAACGAGAAGACGAAGCCGCTCGTGCCTACGAC  300

Qy     392  GTCGCGGTTCACAGGTTCCGTCGCGTGACGCCGTCACAAATTCAAAGACGTGAAGATG  451
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  GTCGCGGTTCACAGGTTCCGTCGCGTGACGCCGTCACAAATTCAAAGACGTGAAGATG  360

Qy     452  GACGAAGACGAGTCGATTCTGATTTCTTGAATTCTCATTCGAAATCTGAAATCTGAATATGTTG  511
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  GACGAAGACGAGTCGATTCTGATTTCTTGAATTCTCATTCGAAATCTGAAATCTGAATATGTTG  420

Qy     512  AGGAAACATACTTATAACGAAGAGTTAGAGCAGCAGAGTAAACGGCGTCGTAATGTGTAACGGA  571
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  AGGAAACATACTTATAACGAAGAGTTAGAGCAGCAGAGTAAACGGCGTCGTAATGTGTAACGGA  480

Qy     572  AACATGACTAGGACGTTGTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGG  631
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  AACATGACTAGGACGTTGTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGG  540

Qy     632  TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAGCTA  691
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAGCTA  600

Qy     692  AACCGTTTGGTTGTTATACCGAAACATCACCGCAGAGAAACATTTTCCGTTACCGTCAAGTAAC  751
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  AACCGTTTGGTTGTTATACCGAAACATCACCGCAGAGAAACATTTTCCGTTACCGTCAAGTAAC  660

Qy     752  GTTTCCGTTGAAAGGAGTGTGTTGAACTTTGAACGTTAACGGAAAGTGTGGAGGTTC  811
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  GTTTCCGTTGAAAGGAGTGTGTTGAACTTTGAACGTTAACGGAAAGTGTGGAGGTTC  720

Qy     812  CGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGGTTC  871
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  CGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGGTTC  780

Qy     872  GTTAAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCGTCAG  931
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  GTTAAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCGTCAG  840

Qy     932  GATCAACAGTTGTACATTGGGTGGAAGTCGGATCGGAGTCGGGTCGG  991
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  GATCAACAGTTGTACATTGGGTGGAAGTCGGATCGGAGTCGGGTCGG  900

Qy     992  GTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGTTAACATTCACCGGAGTTGGTGTTGGTGGTGTGTAGCAACGCACGTCGTAGGA  1051
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  GTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGTTAACATTCACCGGAGTTGGTGTTGGTGGTGTGTAGCAACGCACGTCGTAGGA   960

Qy    1052  AACAAAAGAGTGAACGATACTGAGATGTTATCGTTCGTTGGTGTGTAGCAAGAAGCAACGCATC  1111
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  AACAAAAGAGTGAACGATACTGAGATGTTATCGTTCGTTGGTGTGTAGCAAGAAGCAACGCATC  1020

Qy    1112  TTTCACGCCTCGTAA  1126
            |||||||||||||||
Db    1021  TTTCACGCCTCGTAA  1035
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RESULT 7
ATH441073
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LOCUS       ATH441073               1002 bp    mRNA    linear    PLN 15-APR-2002
DEFINITION  Arabidopsis thaliana mRNA for putative auxin response factor 14
            (arf14 gene).
ACCESSION   AJ441073
VERSION     AJ441073.1  GI:20152523
KEYWORDS    arf14 gene; auxin response factor 14.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Carabelli,M., Ciarbelli,A.R., Ruzza,V., Sessa,G., Steindler,C. and
            Ruberti,I.
  TITLE     Nucleotide sequence of the putative Arabidopsis ARF14
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1002)
  AUTHORS   Ruzza,V.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-APR-2002) Ruzza V., Centro di studio per gli Acidi
            Nucleici, Consiglio Nazionale delle Ricerche, c/o Dip. Genetica e
            Biologia Molecolare, Universita La Sapienza, P.le Aldo Moro 5,
            00185 Rome, ITALY
FEATURES             Location/Qualifiers
     source          1..1002
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /cultivar="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="3"
     gene            1..1002
                     /gene="arf14"
     CDS             1..1002
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                     /codon_start=1
                     /evidence=experimental
                     /product="putative auxin response factor 14"
                     /protein_id="CAD29641.1"
                     /db_xref="GI:20152524"
                     /db_xref="GOA:Q9LS06"
                     /db_xref="UniProt/TrEMBL:Q9LS06"
                     /translation="MDAMSSVDESSTTTDSIPARKSSSPASLLYRMGSGTSVVLDSEN
                     GVEVEVEAESRKLPSSRFKGVVPQPNGRWGAQIYEKHQRVWLGTFNEEDEAARAYDVA
                     AHRFRGRDAVTNFKDTTFEEEVEFLNAHSKSEIVDMLRKHTYKEELDQRKRNRDGNGK
                     ETTAFALASMVVMTGFKTAELLFEKVTPSDVGKLNRLVIPHQAEKHFPLPGNNNV
                     SVKGMLLNFEDVNGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKRLCAGDLISFKRSND
                     QDQKFFIGWKSKSGLDLETGRVMRLFGVDISLNAVVVKETEVLMSSLRCKKQRVL"
ORIGIN

Query Match       39.6%;  Score 517.8;  DB 8;  Length 1002;
Best Local Similarity   76.6%;  Pred. No. 2.7e-103;
Matches 719;   Conservative 0;   Mismatches 172;   Indels 48;   Gaps 5;

Qy     100  GAGTAGCGTTGATGAGACGAGAGAGCTTCCATCTGTGAAACCCGGGGATAAC  159
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Db      12  GAGTAGCGTAGACGAGCTTCCTACAACTACAGATTCCATTCCGGCAGAAAGTCATCGTC   71
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REFERENCE    1  (bases 1 to 1242)
AUTHORS      Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
             Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE        Full-length messenger RNA sequences greatly improve genome
             annotation
JOURNAL      Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE      22088475
PUBMED       12093376
REFERENCE    2  (bases 1 to 1242)
AUTHORS      Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
             Feldmann,K.
TITLE        Full-length cDNA from Arabidopsis thaliana
JOURNAL      Unpublished
REFERENCE    3  (bases 1 to 1242)
AUTHORS      Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
             Feldmann,K.
TITLE        Direct Submission
JOURNAL      Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
             Malibu, CA 90265, USA
COMMENT      This clone sequence is one of 5,000 Ceres full-length cDNAs made
             available to TIGR and Genbank. The following quality assessment of
             this set was done by comparison with known proteins: two percent of
             the clones are estimated to be 5'-truncated; less than one percent
             are 3'-truncated; approximately two percent represent alternative
             splice variants, including unspliced introns and spliced exons; one
             percent may contain premature stop codons; five percent may have
             frame shifts in a coding region. A sequence is considered to be
             5'-truncated if it lacks the translation initiation start (ATG). A
             sequence is considered to be 3'-truncated if it lacks the
             C-terminal end of the encoded protein. Please note that these cDNA
             sequences are derived from the Ws or Laer ecotypes and therefore
             may contain polymorphisms when compared to sequences from Col-0.
             Genset carried out the library production and sequencing of the
             full-length clones. Ceres, Inc. carried out the clustering of the
             5' sequences, selection of clones, and sequence assembly.
FEATURES             Location/Qualifiers
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                     SVKGMLLNFEDVNGKVWRPRYSYWNSSQSYVLTKGWSRFVKEKRLCAGDLISFKRSND
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ORIGIN
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Query Match             39.6%;  Score 517.8;  DB 8;  Length 1242;
Best Local Similarity   76.6%;  Pred. No. 2.7e-103;
Matches  719;  Conservative  0;  Mismatches 172;  Indels 48;  Gaps  5;
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Qy   100  GAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAAC  159
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Db    97  GAGTAGCGTAGACGAGAGCTCACAACTACAGATTCCATTCCGGCGAAGTCATCGTC      156

Qy   160  TCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGGTTGT  219
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Db    72  TCCGGCGA----------GTTACTACTATATAGAATGGGAAGCCGGAACAAGCGTGGT     116

Qy   220  GTTAGATTCAGAGAACGGCGTA----------GAAGCTGAATCTAGGAGCCTTCCGTC      267
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Db   117  ACTTGATTCAGAGAACCGGGTGTCGAAGTCGAAGTCGGGAGCTCAGATTTACGA        176

Qy   268  GTCAAAATACAAAGGTGGTGGTGCCACAACCAAACGAAGATGGGGAGCTCAGATTTACGA  327
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Db   177  TTCAAGATTCAAAGGTGTGTTCCTCAACGAAGAAAAGCTTCCTTC                 236

Qy   328  GAAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGGAGACCGAAGCCGCTCGTGCCTA  387
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Db   237  GAAACATCAACGCGTGTGGCTTGGCTTGTGTACTTTCAACGAGGAGCAGCCTCGTGCTTA   296

Qy   388  CGACGTCGCGGTTCACAGGTTCCGTCGCGCCGTGACGCCCGTCACAAATTTCAAGACGTGAA  447
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Db   297  CGACGTCGCGGCTCACCGGTTCCGTCGGGCCGATGCCCGTTACTAATTTCAAAGAC---AC   353

Qy   448  GATGGACGAAGAGGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATAT             507
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Db   354  GACGTTCGAAGAGAGGTTGAGTTCTTAAACGGCCATTCGAAATCAGAGAATCAGATTAT    413

Qy   508  GTTGAGGAGAACATACTTATAACGAAGAGTTAGACGCAGAGTAAACGGCGTCGTAATGGTAA  567
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Db   414  GTTGAGAAAACACACTTACAAGAAGAAGAGTTAGACCGGTCGAAGTCGAAGTCGGCGGTAA  473

Qy   568  CGGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGAC  627
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Db   474  CGGAAAAGAGACGACGCGGGCGTTGCTTTGGCTTGCGATG----------GTGGTTATGAC  521

Qy   628  GGGGTTAGATCGGCGGAGGCACTGTTGAGAAAGCCGGTAACGCCAAGCGACGTTGGGAA  687
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Db   522  GGGGTTAAAACGCGGAGTACTGTTTGAGAAAACGTAACGCCAAGTGACGTTCGGGAA     581

Qy   688  GCTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCA--   745
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Qy   746  ----AGTAACGTTCCGTGAAAGGAGTGTTGTTGCAGTCAGAGCGTTAACGGGGAAAGT  801
              |||| |||| ||| ||||| | |||| |   || || |  ||| ||  |||||||
Db   642  TAATAATAACGTCTCGTTAAAGGTATGCGTTGAATTTCGAAATGTTTCGAAGGGGAAAGT   701

Qy   802  GTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTCAGACTAAAGGTTG  861
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Db   702  GTGGAGGTTCCGTTACTCGTATTGGAATAGTAGTCAAAGTTATGTGTTGGACCAAAGGTTG   761

Qy   862  GAGCAGGTTCGTTAAGGAGAAGAATCTACGTGTCGGTGGTTAGTTTCAGTAGATC  921
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Db   762  GAGTAGATTCGTTAAAGAGAAGAGAGACCTTGTGTCTGTGATTTGATCAGTTTAAAAGATC   821

Qy   922  TAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGA  981
          || |||||| |||||||| || |  |||  ||||| |||| ||||| |||| ||||| ||
Db   822  CAACGATCAAGATCAAAGATCAAAAATTCTTTATCGGGTGGAAATCGAAATCGGGGTTGGATCTAGA  881

Qy   982  TGCGGGTCGGGTTTTGAGATTGTTCGGAGTTGGGGTTAACATTTC  1020
          || | || |||| ||||||| || ||| ||| |||| |  ||||
Db   882  GACGGGTCGGGTTATGAGATTGTTTGGGGGTTGATATTTC                      920
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RESULT 8
AY087951
LOCUS       AY087951                1242 bp    mRNA    linear   PLN 14-APR-2003
DEFINITION  Arabidopsis thaliana clone 39877 mRNA, complete sequence.
ACCESSION   AY087951
VERSION     AY087951.1  GI:21406725
KEYWORDS    FLI cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
```

JOURNAL   Submitted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research
           Institute, Department of Plant Gene Research; 1532-3, Yana,
           Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
           Tel:81-438-52-3935, Fax:81-438-52-3934)

COMMENT   Address for correspondence: kaos@kazusa.or.jp
           For the latest information on annotation of this clone, please see
           http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=K13N2
           Genes with similarity to proteins in the databases are described in
           'product' or 'note' qualifiers. Genes that have no significant
           protein similarity are described as 'unknown protein'.
           The software programs used to predict genes include: Grail
           (Informatics Group, Oak Ridge National Laboratory,
           http://compbio.ornl.gov/Grail-1.3/),
           GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
           NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
           Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
           SplicePredictor (Volker Brendel, Stanford University,
           http://gremlin1.zool.iastate.edu/cgi-bin/sp.cgi).
           Genes encoding tRNAs are predicted by tRNAscan-SE
           (Sean Eddy, Washington University School of Medicine, St. Louis,
           http://genome.wustl.edu/eddy/tRNAscan-SE/).
           This sequence may not be the entire insert of this clone. It may be
           shorter because we remove overlaps between neighboring submissions.
           The 5' clone is T5M7 and the 3' clone is K9I22.

FEATURES   Location/Qualifiers
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Qy   328 GAAACACCAGCGCGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTA 387
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Db   322 GAAACATCAACGCGTGTGGCTTGGCTACTTTCAACGAGGAAGACGAAGCCAGCTGTGCTTA 381

Qy   388 CGACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAGACGTGAA 447
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Db   382 CGACGTCGCGGTTCACCGTTCCCGGCGCCGGATGCCGTTACTAATTTCAAAGAC---AC 438

Qy   448 GATGGGACGAAGACGACGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATAT 507
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Db   439 GACGTTCGAAGAAGAGGTTGAGTTCTTAAACGGCATTCGAAATCAGAGATCGTAGATAT 498

Qy   508 GTTGAGGAAACATACTTATAACGAAGAGTTAGAGCGAGCAGTAAACGGCCGTCGTAATGGTAA 567
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Qy   568 CGGAAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTCTACGAC 627
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Qy   628 GGGGTTTAGATCGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCCAAGCGACCTTGGGAA 687
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Db   607 GGGGTTTAAAACGGCGAGTACTGTTTGAGAAAAACCGGTAACCGTAACCGCCAAGTGACGTCGGGAA 666

Qy   688 GCTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCA-- 745
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Db   667 ACTAAACCGTTTAGTTATACCAACAAAACACCAAGCCGAGAAACATTTTCCGTTACCGTTAGG 726

Qy   746 ---AGTAACGTTTCCGTGAAAGGAGTGTGTTGAACTTGTTGTTGAGGACGTTAACGGAAAGT 801
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Qy   802 GTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTAGTTGTTTGACTAAAGGTTG 861
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Qy   922 TAACGGTTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAAATCTCAGATTTAGA 981
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RESULT 9
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LOCUS   AB028607   77483 bp   DNA   linear   PLN 14-FEB-2004
DEFINITION Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K13N2.
ACCESSION   AB028607 BA000014
VERSION   AB028607.1 GI:5041960
KEYWORDS   .
SOURCE   Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.
  TITLE   Structural analysis of Arabidopsis thaliana chromosome 3. I.
            Sequence features of the regions of 4,504,864 bp covered by sixty
            P1 and TAC clones
  JOURNAL   DNA Res. 7 (2), 131-135 (2000)
   MEDLINE   20277480
   PUBMED   10819329
REFERENCE   2 (bases 1 to 77483)
  AUTHORS   Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E. and Tabata,S.
  TITLE   Direct Submission

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Qy    100  GAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAAC  159
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Db  33212  GAGTAGCGTAGACGAGAGCTCTACAACTACAGATTCCATTCCGGCGGAGAAAGTCATCGTC  33271

Qy    160  TCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAGCGGATCAAGCGTTGT  219
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Db  33272  TCCGGCGA-----------GTTACTATATAGAAATGGAACGGAGCGGACAAGCGTGGT  33316

Qy    220  GTTAGATTCAGAGAACGGCGTA-----------GAAGCTGAATCTAGGAAGCTTCCGTC  267
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Db  33317  ACTTGATTCAGAGAACGGGTGCGAAGTCGAAGTCGAAGCCGAATCAAGAAAGCTTCCTTC  33376

Qy    268  GTCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTACGA  327
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Qy    328  GAAACACCAGCGCGTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTA  387
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Db  33437  GAAACATCACGCGCGTGTGGCTCGGACTGTTGTTCAACGAGGAAGCAGCTCGTGCTTA  33496

Qy    388  CGACGTCGCGGTTCACAGGTTCCGTCGCCGTTGACCGTCGATGCTCACAAATTCAAAGACGTGAA  447
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Db  33497  CGACGTCGCGGCTCACCGTTTCCGTGGCCGCGATGCCGTTACTAATTTCAAAGAC---AC  33553

Qy    448  GATGGACGAAGACGAGGTCGCGATTCTGAATTCTCATTCGAAATCTGAGATCGTTGATAT  507
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Db  33554  GACGTTCGAAGAAGAGGTTGAGTTCTTAAACGCGCATTCGAAATCAGAGATCGTTAGATAT  33613

Qy    508  GTTGAGGAAACATACTTATAACGAAGAGTTAGACAGAGTAAACGGCGTCGTAATCGTAA  567
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Db  33614  GTTGAGAAAACACACTTACAAGAAGAAGAGTTAGACCAAAGGAAACGTAACCGTGACGGTAA  33673

Qy    568  CGGAAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGAC  627
           |||||||||||||  |||||||  ||||||||||||||||              |
Db  33674  CGGAAAAGAGAGACGACCGCGTTTGCTTTGGCTTGGATG---------------GTGGTTATGAC  33721
```

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JOURNAL     Submitted (23-SEP-2002) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
COMMENT     RIKEN Genomic Sciences Center (GSC) members carried out the
            collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
            Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
            Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
            Hayashizaki,Y. and Shinozaki,K.

            The Salk, Stanford, PGEC (SSP) Consortium members carried out the
            sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan,M.M.,
            Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M., Quach,H.L.,
            Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yu,G.,
            Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M.,
            Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,
            Ecker,J.R. and Theologis,A.

            Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
            this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
            contributed equally to this work as PIs.
FEATURES             Location/Qualifiers
     source          1..1279
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /chromosome="1"
                     /clone="RAFL08-13-K22 (R11283)"
                     /ecotype="Columbia"
                     /note="This clone is in a modified pBluescript vector
                     (FLC-1) as a BamHI/XhoI insert."
     gene            1..1279
                     /gene="Atlg25560"
     misc_feature    66..1149
                     /gene="Atlg25560"
                     /note="This may be a potential full length cDNA
                     corresponding to gene Atlg25560. The cDNA contains a two
                     base pair deletion (GG) between positions 756 and 757
                     resulting in a truncated ORF."
     misc_difference 756..757
                     /gene="Atlg25560"
                     /note="compared to genomic sequence"
                     /replace="ggga"
     misc_difference 1263
                     /gene="Atlg25560"
                     /note="not present in genomic sequence"
ORIGIN

Query Match           30.1%;   Score 393.2;   DB 8;   Length 1279;
Best Local Similarity 64.5%;   Pred. No. 6.9e-76;
Matches  673;   Conservative   0;   Mismatches  328;   Indels  43;   Gaps  4;

Qy    159 CTCCGGCGAAAAGTCGTCGGGTAGGTAACTTATACAGGATGGGAAGCCGATCAAGCGGTTG 218
          ||||||   || || ||||||||||||||  ||||||| |||||||| |||||||||||||
Db    163 CTTCTCCGGCCGGCGACGTCGATGCGTCTCTACAGAATGGGAAGCGGCCGGAAGCGCGTCG 222

Qy    219 TGTTAGATTCAGAGAACGGCGTAGAAGCTTCCGTCGTCAAAATACA 278
          | |||| ||||||| ||| ||||  |||| || ||||||||||||||
Db    223 TTTTGGATTCAGAGAACGGCGTCGAGACCGCACGAGTAAGCTTCCGTTCGTCGAAATATA 282

Qy    279 AAGGTGTTGGTGCCACAACCAACCAAACGGAAGATGGGGAGTTCAGATTTACGAGAAACACCAGC 338
          |||||||||| ||| |||||| || | ||| |||||||||||||||||||| ||||||||||||||
Db    283 AAGGCGTTGTGCCTCAGCTAACGGAAGACGAAGAAGGGGAGTTCAGATTTACGAGAAGCATCAGC 342

Qy    339 GCGTGTGCTGGCGGACATTCAACGAGGCCGCTCGGTCGTCGGCCTACGACGTCGCGG 398
          ||| |||||||| |||| |||| ||||| | |||| |  ||||| |||||||||||||
Db    343 GAGTTTGGCTCGTTACTTCAACGAGGAAGAAGAAGTTGCGTCTTCTTACGATCGGCCG 402

Qy    399 TTCACAGGTTCCGTCGCCGTCGACGGCCGTCACAAATTTCAAA---GACGTGAAGATGACG 455
          ||||||| |||||| || || || ||||||||||  |||| ||| ||||||||||||||||
Db    403 TGAGGAGATTCCGCGACGGCCGGCCCGTCACTACTTCAAATCTAACTTCAAATCTCAAGTTGATGGAAACG 462

Qy    456 AAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGATCGGTTCAGATCGTTGAGGA 515
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        Qy    628 GGGGTTTAGATCGGCGGAGGCACTCGTTGAGAAAGCCGTAACCGGCACGTGCGGAA 687
                  ||||||| |   || || ||| ||||||||||||||||||||||||||||||||||
        Db  33722 GGGGTTTAAAACGGCGGAGTTACTCGTTTGAGAAAACCGTAACCGCCAAGTGACGTCGGGAA 33781

        Qy    688 GCTAAACCGTTTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCA-- 745
                  |||  |||||||| || |||||| |||| ||||||| |||||||||||||||||||||
        Db  33782 ACTAAACCGTTTTAGTTATACCAAAACACACCAAGCGGAGAAACATTTCCGTTACCGTTAGG 33841

        Qy    746 ----AGTAACGTTTCCGTGAAAGGAGTGTGTTGAAACTTGAGACGTTAACGGGAAAGT 801
                  ||||||| ||||||||||||  || |||  ||||||||||||||||||
        Db  33842 TAATAATAACGTTCTCCGTAAAGGTATGCTGTTGAATTTCGAAGACGTTAACGGGAAAGT 33901

        Qy    802 GTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTAGTTTTGACTAAAGGTTG 861
                  ||||||||||||||||||||||| || ||| || ||| ||| ||||| |||||||||||
        Db  33902 GTGGAGGTTCCGTTACTCTTATTGGAATAGTAGTCAAAGTAGTATGTGTTGACCAAAGGTTG 33961

        Qy    862 GAGCAGGTTCGTTAAGGAAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATC 921
                  |||||||||||||||| || ||||||||||| |||| |||| ||  ||  || ||| ||||
        Db  33962 GAGTAGATTCGTTAAAGAAGAAGAGAGACTTTGTGCTGCGGTGATTTCATCAGTTTTAAAAGATC 34021

        Qy    922 TAACGGTCAGATCAACAGTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGA 981
                  |||| |||||||| ||||||| || || ||||||||||||  || ||||||||||||||
        Db  34022 CAACGATCAAGATCAAAATTCTTTATCTGGGGTGAAATCGAAATCCGGGTTGGATCTAGA 34081

        Qy    982 TGCGGGTCGGGTTTTGAGATTGTTCGGAGTTAACATTTC 1020
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RESULT 10
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LOCUS       AY056169                1279 bp    mRNA      linear       PLN 23-SEP-2002
DEFINITION  Arabidopsis thaliana Atlg25560 mRNA sequence.
ACCESSION   AY056169
VERSION     AY056169.1  GI:15810260
KEYWORDS    FLI CDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1279)
  AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
            Lee,J.M., Quach,H.L., Tang,C., Toriumi,M., Wallender,E.K., Wong,C.,
            Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R.,
            Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J.,
            Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
            Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,
            Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Arabidopsis Full Length cDNA Clones
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1279)
  AUTHORS   Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M.,
            Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y.,
            Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R.,
            Hayashizaki,Y., Ishida,J., Kamiya,A., Karlin-Neumann,G.,
            Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C.,
            Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
            Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E.,
            Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Arabidopsis Full Length cDNA Clones
  JOURNAL   Direct Submission
            Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan
            Street, Albany, CA 94710, USA
REFERENCE   3  (bases 1 to 1279)
  AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
            Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wallender,E.K.,
            Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R.,
            Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J.,
            Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
            Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K.,
            Davis,R.W., Ecker,J.R. and Theologis,A.
  TITLE     Direct Submission
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           TITLE      Arabidopsis Full Length cDNA Clones
           JOURNAL    Unpublished
           REFERENCE  2  (bases 1 to 1376)
           AUTHORS    Yamada,K., Banh,J., Chan,M.M., Chang,E., Dale,J.M.,
                      Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
                      Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
                      Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
                      Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
                      Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
                      Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
                      Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
           TITLE      Direct Submission
           JOURNAL    Submitted (21-MAR-2002) Plant Gene Expression Center, 800 Buchanan
                      Street, Albany, CA 94710, USA
           COMMENT    RIKEN Genomic Sciences Center (GSC) members carried out the
                      collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
                      Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
                      Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                      Hayashizaki,Y. and Shinozaki,K.

                      The Salk, Stanford, PGEC (SSP) Consortium members carried out the
                      sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J.,
                      Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,
                      Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
                      Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,
                      Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
                      Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,
                      Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

                      Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
                      this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
                      contributed equally to this work as PIs.

                      Annotation is based on the January 2002 version of the Arabidopsis
                      genome submitted to GenBank.
           FEATURES           Location/Qualifiers
           source    1..1376
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /chromosome="1"
                     /clone="RAFL09-74-F02 (R19336)"
                     /ecotype="Columbia"
                     /note="This clone is in a modified pBluescript vector
                     (PLC-1) as a BamHI/XhoI insert."
           gene      1..1376
                     /gene="At1g25560"
           5'UTR     1..60
                     /gene="At1g25560"
           CDS       61..1146
                     /gene="At1g25560"
                     /codon_start=1
                     /evidence=experimental
                     /product="putative DNA-binding protein RAV2"
                     /protein_id="AAM13889.1"
                     /db_xref="GI:20259539"
                     /translation="MEYSCVDDSSTTSESLSISTTPKPTTTBKKLSSPPATSMRLYR
                     MGSGGSSVVLDSENGVETESRKLPSSKYKGVVPQPNGRWGAQIYEKHQRVWLGTFNEE
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                     EQSRRKFVNGDGKRSGLETATYGNDAVLRAREVLFEKVTPSDVGKLNRLVIPKQHAE
                     KHFPLPAMTTAMGMNPSPTKGVLINLEDRTGKVWRFRYSYWNSSQSYVLTKGWSRFVK
                     EKNLRAGDVVCFBRSTGPDRQLYIHWKVRSSPVQTVVRLFGVNIFNVSNEKPNDVAVE
                     CVGKKRSREDDLFSLGCSKKQAIINIL"
           3'UTR     1147..1376
                     /gene="At1g25560"

           ORIGIN
           Query Match           29.9%;    Score 391.2;  DB 8;  Length 1376;
           Best Local Similarity 64.3%;    Pred. No. 1.9e-75;
           Matches  673;         Conservative  0;  Mismatches 328;  Indels 45;  Gaps  4;

           Qy    159  CTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACACGGATCGGAAGCGGATCAAGCGTTG  218
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           Db   463  ACGCGGCGAATCGGCTTTCTTGACCTCATTCTAAAGCTGAGATCGTCGGATATGTTGAGGA  522
                      | ||  |  || ||| ||   |   || || |  |||  |||| | |||| || ||||
           Qy   516  AACATACTTATAACGAAGCTTAGAGCAGAGAGTAAACGGCGTCGTCCTAATGGTAACGGAAACA  575
                      ||||    ||||    | ||||||||| ||||||||| ||||||  |||||
           Db   523  AACACACTTACGCCGATGAGTTTGAGCGAGTAGACGGAAGTTTGTTAACGGACCGAA  582
                      |||
           Qy   576  TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTTA  635
                      |||||          ||| ||  ||     |||  |    |||
           Db   583  AACGGCTCTGGGTTGGAGACGCGGCGACGTACGGAAACGACGCGTGTT---------TTGA  630
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           Qy   636  GATCGGCGGAGGCACTGTTGAGAAAGCGGTAACGCCAAGCGACGTGGGAAGCTAAACC  695
                      ||||||| || ||||||| |||  |  ||||||| || ||||| | || ||| ||||
           Db   631  GAGCGGCGTGAGGTTTTGTTCGAGAAGACTGTTACGCCCGAGCGTCGGAAGCTGAACC  690
                      ||| ||||  ||| ||||| |||||   |||||||  ||||  |  ||| ||| ||||
           Qy   696  GTTTGGTTATACCGGAAACATCACGCAGCAGAAACATTTTCCGTTACCGTCAAGTAACGTTT  755
                      |||||| ||||| |||||| ||| ||||| ||||||||||||||||  |||||| ||||
           Db   691  GTTTAGTGATACCGGAAACAACACGCGGAAGCATTTTCCGTTACCGGCGATGACGACGG  750
                      |||| || ||||| ||||| ||||| ||| ||||||||||| | ||||| ||| ||||
           Qy   756  CCGT----------------GAAAGGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGG  796
                                          ||| | |||| || || || |||  |   |||  ||||
           Db   751  CGATGGATGAATCCGTCTCCGACGAAAGGCGTTTGATTAACTTGGAAGATAGAACAGGG  810
                      || ||  | ||||  || |   |  |||| |  | |||  |||| || |  ||||||||
           Qy   797  AAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGATTTGTGACTAA  856
                      |||||||| |||| |||| | ||| ||||| || ||||| ||| |||  |||||
           Db   811  AAAGTGTGCGGGTTCCGTTACGTCACAGTCCAGTCAAACGTTACCGTGTTGACCAAG  870
                      |||||||| ||||||||| | | ||  ||| || ||||  ||||| |||  |||||
           Qy   857  GGTTGGGAGCAGGTTCGTTAAGGAGGAGAATCTACGTGCTGGTGACGTCGGTTCAGT  916
                      ||||| ||||||| | ||| |||||| ||  ||||| || |||||| |  ||||||
           Db   871  GGCTGGGAGCCGGTTCGTTAAAGAGAAGAATCTTCGAGCCGGTGATGTGTTTCGAG  930
                      || ||||||| |||| || ||  ||| ||||||| ||  ||||| ||||  |||||
           Qy   917  AGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCGCAGAT  976
                      || ||||  |||| |||| |||| ||| || ||| |||||||||| ||| |||||
           Db   931  AGATCAACCAGCCAGACGCGGCAATTGTATATCCACTGGAAAGTCCGGTCTAGTCCGGTT  990
                      |||| |  | | |||| | |||||||||| | | ||||| ||| |||| ||| |||||
           Qy   977  TTAGATGCGGGTCGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGA  1036
                      |||||| ||| || ||| || ||| |||| ||||| || ||| ||||| || |||||
           Db   991  CAGACTGTGTGTTAGCGTATTCGGACTCAACATTTTCAATGTGAGTAACGAGAAACCAAAC  1050
                      ||||| ||| || ||| |||| |||  ||||||||| | |||| || |||||| ||||
           Qy  1037  AACGACGTCGTA---------GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTGTG  1087
                      |||| |||| |          |||||  ||| |||||| ||   |||| |||| ||||
           Db  1051  GACGTCCGAGTAGAGTGTGTTGGCAAGAAGAGATCTCGGGAAGATGATTTGTTTTCGTTA  1110
                      |||| | ||||||||| || ||| ||||| |||| ||| ||| ||  |||||| |||||
           Qy  1088  GTGTGTAGCAAGAAGAGCAAACGCCATCTTCACGCCCTGTAACAACTCTTCTTCTTTTTTT  1147
                      ||||| |||||||| |  |||| |||||| |||  ||  |||||  ||||||||||||||
           Db  1111  GGGTGTTCCAAGAAGCAGGCGGCGATTATCAACATCTTGTGACAAATTCTTTTTTTTGGTTT  1170
                      ||||||| ||||||  ||| ||||| |||| ||| | || | | |||||||||||| |||
           Qy  1148  TCTTTTGTTGTTTTAATAATTTTT  1171
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           Db  1171  TTTTTCTTCAATTTGTTTCTCCTT  1194
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           RESULT 11
           AY091069
           LOCUS       AY091069      1376 bp    mRNA      linear    PLN 18-SEP-2002
           DEFINITION  Arabidopsis thaliana putative DNA-binding protein RAV2 (At1g25560)
                       mRNA, complete cds.
           ACCESSION   AY091069
           VERSION     AY091069.1  GI:20259538
           KEYWORDS    FLI_CDNA.
           SOURCE      Arabidopsis thaliana (thale cress)
           ORGANISM    Arabidopsis thaliana
                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                       rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
           REFERENCE   1  (bases 1 to 1376)
           AUTHORS     Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
                       Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
                       Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
                       Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
                       Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
                       Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
                       Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
                       Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
```

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LOCUS        AC079281    102540 bp    DNA    linear    PLN 19-JAN-2001
DEFINITION   Arabidopsis thaliana chromosome 1 BAC F2J7 genomic sequence,
             complete sequence.
ACCESSION    AC079281
VERSION      AC079281.4  GI:12321495
KEYWORDS     HTG.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE    1 (bases 1 to 102540)
  AUTHORS    Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
             Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
             Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
  TITLE      Arabidopsis thaliana chromosome 1 BAC F2J7 genomic sequence
  JOURNAL    Unpublished
REFERENCE    2 (bases 1 to 102540)
  AUTHORS    Town,C.D. and Kaul,S.
  TITLE      Direct Submission
  JOURNAL    Submitted (26-AUG-2000) The Institute for Genomic Research, 9712
             Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
REFERENCE    3 (bases 1 to 102540)
  AUTHORS    Town,C.D. and Kaul,S.
  TITLE      Direct Submission
  JOURNAL    Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
             Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
             On Jan 19, 2001 this sequence version replaced gi:12280814.
COMMENT      Address all correspondence to:at@tigr.org

             BAC clone F2J7 is from Arabidopsis thaliana chromosome 1
             The orientation of the sequence is from SP6 to T7 end of the BAC
             clone.
             Genes were identified by a combination of several methods: Gene
             prediction programs including Genscan+ (Chris Burge,
             http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
             http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
             of GlimmerM, see Mihaela Pertea,
             http://www.tigr.org/softlab/glimmerm/glimmerm_htm.html, and
             GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
             mpertea@tigr.org), searches of the complete sequence against a
             peptide database and the plant EST database at TIGR
             (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
             indicate the level of evidence for their annotation. Genes with
             similarity to other proteins are named after the database hits.
             Genes without significant peptide similarity but with EST
             similarity are named as unknown proteins. Genes without protein
             or EST similarity, that are predicted by more than two gene
             prediction programs over most of their length are annotated as
             hypothetical proteins. Genes encoding tRNAs are predicted by
             tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
             Simple repeats are identified by repeatmasker (Arian Smit,
             http://ftp.genome.washington.edu/RM/RepeatMasker.html).
FEATURES             Location/Qualifiers
     source          1..102540
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Columbia"
                     /db_xref="taxon:3702"
                     /chromosome="I"
                     /map="?"
                     /clone="F2J7"
     repeat_region   complement(356..382)
                     /rpt_family="(CATTA)n"
     repeat_region   complement(421..495)
                     /rpt_family="AT_rich"
     repeat_region   complement(897..1021)
                     /rpt_family="AT_rich"
     gene            2262..3272
                     /gene="F2J7.1"
                     /note="similar to hypothetical protein GI:7269821 from
                     (Arabidopsis thaliana)"
     mRNA            join(<2262..2360,2452..2638,2728..
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Db  158  CTTCTCCGCGGCGACGTCGATGCGTCTCCTACAGAATGGGAAGCGGCGGAAGCAGCGTCG   217
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Qy  219  TGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACA   278
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Db  218  TTTTGGATTCAGAGAACGGCCGTCGAGACCGAGTCACGTAAGCTTCCTTCGTCGAAATATA  277

Qy  279  AAGGTGTGTGCCACAACCACCAGCGGAAGATGGGGAGCTCAGATTTACGAGAAACACCAGC   338
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Db  278  AAGGCCGTTGTGCCTCAGCCTAACCGGAAGATGGGGAGCTCAGATTTACGAGAAGCATCAGC  337

Qy  339  GCGTGGCTGCCTCGGGACATTCAACGAAGAGAACCGAAGCCGCTCGTGCCTACGACGTCGCGG   398
         |  |||||| || |  |||||||||| | | ||  | || ||| ||  |||| ||||| |||||
Db  338  GAGTTTGGCTCCGTACTTTCAACCAACGAAGAAGCTGCGTCTTCTTCCTACGACATCGCCCG  397

Qy  399  TTCACAGTTCCGTCGCCGTGACGCCCGTCACAAATTTCAAA---GACGTGAAGATGACG   455
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Db  398  TGAGGAGATTCCCGCGGCCGCGACCCGTCACTAACTTCAAATCTCAAATTCAAGTTGATGGAAACG  457

Qy  456  AAGACAGGAGGTCGATTTCTTGAATTCTCATTCGAGAATCGTGTGATATGTTGAGGA   515
         | |  ||   ||| ||||||||||  || |||||||||||  ||||| |||||||||
Db  458  ACGCCGAATCGGCTTTTCTTGACGCTCATTCTAAAGCTGAGATCGTCGGATATGTTGAGGA  517

Qy  516  AACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGACGAAACA   575
         |||| |||||  |||| |||| ||||||||||| |||  || |||  | ||| |||||||||||
Db  518  AACACACTTACCGCGATGAGTTTGAGCAGAGTAGACGAGAAGTTGTTAACGGCGACGAA  577

Qy  576  TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTTA   635
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Db  578  AACGGCTCTGGGTTGGAGACGCGGCCACGTACGGGAAACGACGCTGTT------TTGA  625

Qy  636  GATCGCGCGGAGGCCACTGTGTTGAGAAAGCGGTAACGCGCCAAGCGACGTGGGAGCTAAACC   695
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Db  626  GAGCGCGTGAGGTTTGTTGTTCGAGAAGACTGTTACGCCGAGCACGCTCGGGAAGCTGAACC  685

Qy  696  GTTTGGTTATACCGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAGTAACGTTT   755
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Qy  756  CCGT----------GAAAGGAGTGTGTTGAACTTTGAGGACGTTAACG   794
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Qy  795  GGAAAGTGTGGAGGTTCCGTTCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTA   854
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Db  806  GGAAAGTGTGGCGGCGTTCCGTTCCGTTACAGTTACTGGAACAGCAGTCAAAGTTACGTGTTGACCA  865

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Db  1106 TAGGGTGTTCCAAGAAGCAGGCGATTATCAACATCTTGTGACAAATTCTTTTTTTTTGGT  1165

Qy  1146 TTTCTTTTGTTGTTTTAATAATTTTT   1171
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RESULT 12
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Best Local Similarity  64.3%;   Pred. No. 2.6e-75;
Matches  673;     Mismatches  328;   Conservative  0;   Indels  45;   Gaps  4;

Qy     159 CTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCAAGCGGTTG 218
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Db   18375 CTTCTCCGCCGCGACGTCGCATGCGTCTCTACAGAATGGGAAGCCGCGGAAGCAGCGGTCG 18434

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```
AUTHORS    Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
           Lee,J.M., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yu,G.,
           Bowser,L., Carninci,P., Chen,H., Cheuk,R., Karlin-Neumann,G., Kawai,J.,
           ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
           Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
           Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
           Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE      Arabidopsis Open Reading Frame (ORF) Clones
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 1117)
AUTHORS    Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W.,
           Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yu,G.,
           Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
           ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
           Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
           Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
           Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
TITLE      Direct Submission
JOURNAL    Submitted (17-JUN-2002) Plant Gene Expression Center, 800 Buchanan
           Street, Albany, CA 94710, USA
COMMENT    The RIKEN Genomic Sciences Center (GSC) members carried out the
           collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
           Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., ishida,J.,
           Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J.,
           Hayashizaki,Y. and Shinozaki,K.

           The Salk, Stanford, PGEC (SSP) Consortium members constructed and
           sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada,K.,
           Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Hsuan,V.W., Lee,J.M.,
           Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yu,G., Bowser,L.,
           Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B.,
           Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
           Davis,R.W., Ecker,J.R. and Theologis,A.

           Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
           to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP
           /PGEC) contributed equally to this work as PIs.

           Annotation is based on the January 2002 version of the Arabidopsis
           genome submitted to GenBank.
FEATURES             Location/Qualifiers
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Qy   399 TTCACAGGTTCCGTCCGTGAGCGCCGTCACAAATTTCAAA---GAGTGAAGATGGACG 455
Db   18615 TGAGGAGATTCCCGCGGCCGCGACGCCGTCACTTCAAATCTCAAGTTGATGGAAACG 18674

Qy   456 AAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCGAGAGATCGTTGATATGTTGAGGA 515
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Db   18735 AACCACTTACGCCGATGAGTTTGAGCGACGGAAAGTTGTTAACCGGCGACGGAA 18794

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RESULT 13
AY122941
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DEFINITION Arabidopsis thaliana putative DNA-binding protein RAV2 (At1g25560)
            mRNA, complete cds.
ACCESSION   AY122941
VERSION   AY122941.1 GI:21689704
KEYWORDS   FLI CDNA.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 1117)

Query Match   29.8%;   Score 389.8;   DB 8;   Length 1117;
Best Local Similarity   64.8%;   Pred. No. 3.8e-75;
Matches   665; Conservative   0; Mismatches   317; Indels   45; Gaps   4;

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RESULT 14
AC011914/c
LOCUS           AC011914            96808 bp    DNA       linear   PLN 19-JAN-2001
DEFINITION      Arabidopsis thaliana chromosome 1 BAC F14K14 genomic sequence,
                complete sequence.
ACCESSION       AC011914
VERSION         AC011914.9  GI:12324129
KEYWORDS        HTG.
SOURCE          Arabidopsis thaliana (thale cress)
  ORGANISM      Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE       1  (bases 1 to 96808)
  AUTHORS       Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
                Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
                Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
  TITLE         Arabidopsis thaliana chromosome 1 BAC F14K14 genomic sequence
  JOURNAL       Unpublished
REFERENCE       2  (bases 1 to 96808)
  AUTHORS       Lin,X. and Kaul,S.
  TITLE         Direct Submission
  JOURNAL       Submitted (16-OCT-1999) The Institute for Genomic Research, 9712
                Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE       3  (bases 1 to 96808)
  AUTHORS       Town,C.D. and Kaul,S.
  TITLE         Direct Submission
  JOURNAL       Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
                Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
COMMENT         On Jan 19, 2001 this sequence version replaced gi:11280763.
                Address all correspondence to:at@tigr.org

                BAC clone F14K14 is from Arabidopsis thaliana chromosome 1
                The orientation of the sequence is from SP6 to T7 end of the BAC
                clone.
                Genes were identified by a combination of several methods: Gene
                prediction programs including Genscan+ (Chris Burge,
                http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
                http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
                of GlimmerM, see Mihaela Pertea,
                http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
                GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
                mpertea@tigr.org), searches of the complete sequence against a
                peptide database and the plant EST database at TIGR
                (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
                indicate the level of evidence for their annotation. Genes with
                similarity to other proteins are named after the database hits.
                Genes without significant peptide similarity but with EST
                similarity are named as unknown proteins. Genes without protein
                or EST similarity, that are predicted by more than two gene
                prediction programs for most of their length are annotated as
                hypothetical proteins. Genes encoding tRNAs are predicted by
                tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
                Simple repeats are identified by repeatmasker (Arian Smit,
                http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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                     /chromosome="1"
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                     /note="similar to bZIP DNA-binding protein GB:AAD55394
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     mRNA            <2580..>2996
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Qy   159  CTCCCGGCGAAAAAGTCGTCGTAGTAACTTATACAGGATGGGAAGCCGATCAAGCGTTG  218
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Db    98  CTTCTCCCGGCCGGCGACGTCGATGCGTCTCTACAGAATGGGAAGCGGCGGAAGCAGCGTCG  157

Qy   219  TGTTAGATTCAGAGAACGGCGTAGAAGCTGAAATCTAGGAAGCTTCCGTCGTCAAAATACA  278
          ||| ||||||||| || |||  ||   ||  || |||   ||||  || ||| |||| |||
Db   158  TTTTGGATTCAGAGAACGGCGCGTCGAGACCCGAGTCACGTAAGCTTCCTTCGTCGAAATATA  217

Qy   279  AAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTTCAGATTACAGAGAAACACCAGC  338
          ||||| ||||||| ||  |||  |||| |||||||| ||||||||||||| ||| |||||
Db   218  AAGGCGTTGTGCCTCAGCTCAACGGAAGATGGGGAGCTTCAGATTTACGGAGAAGCATCAGC  277

Qy   339  GCGTGTGGCTCGGGACATTCAACGAAGAAGACCAAGCCGCTCGTGCCTACGACGTCGCGG  398
          |  |||| |||||| ||||||||| || |||||||| |||  ||||  ||||||||||||
Db   278  GAGTTTGGCTCGGTACTTTCAACGAAGAAGCTGCGTCTCTTCTTACGACATCGCCG  337

Qy   399  TTCACAGGTTCCGTCGTCGCCGTGACCGCGTCACAAATTCAAA---GACGTGAAGATGGACG  455
          ||||||||||| ||||||||||||||||||||||| |||  || ||  |||  || ||||
Db   338  TGAGGAGATTCCGGCGCCGCGACGCCGTCACTAACTTCAAATCTCAAGTTGATGGAAACG  397

Qy   456  AAGACGAGGTCGATTTCTTCAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGA  515
          || | |  |||  |||| |  | |   ||| ||||| |||||||||||| ||||| ||||
Db   398  ACGCCGAATCGGCTTTTCTTCTTGACGCTCATTCTCAAAGCTCTAAAGCTGAGATCGTGGATATGTTGAGGA  457

Qy   516  AACATACTTATAACGAAGAGTTAGACAGAGAAGTAAACGGCGTCGTAAATGGTAACCGAAACA  575
          || |   ||||  |||  |||| || ||||  ||| |||| |   | || ||| ||| || ||
Db   458  AACACACTTACGCCGATGAGTTTGAGCAGAGTAGACGGAAGTTTGTTAACGGCGCACGGAA  517

Qy   576  TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTTTA  635
          |||| |  | ||  ||||||| ||||   | |   |  |  ||   |||| |||  |||
Db   518  AACGGCTCGGGTTGGAGACGTTGGAGACGCGACGTACCGAAACGACGCCGTGTT--------TTGA  565

Qy   636  GATCGGCCGAGGAGGCACTGTTGAGGAAGCCGGTAACGCGACGGTTGGGAAGCTAAACC  695
          ||  |  ||  ||  |||||||  ||| ||  ||||||  |||  ||  ||||  ||  |||
Db   566  GAGCGGCCGTGAGGTTTTGTTGTTCTGGAGAAGACTGTTACGCCGAGCGACGTCGGGAAGCTGAACC  625

Qy   696  GTTTGGTTATACCGGAAACATCACCGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTT  755
          ||||||| ||  |||||  | |  |||||   ||| ||   |||| |  |||||   |||
Db   626  GTTTAGTGATACCGGAAACAACACACCGCGGAGAAGCATTTCCGTTACCGCGGCGATGACGACGG  685

Qy   756  CCGT------------GAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACG  794
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Db   686  CGATGGGGATGAATCCGTCCGACGAAAGCGTTTGATTAACTTGGAAGATAGAACAG  745

Qy   795  GGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTA  854
          ||||||||||  |||| |||| ||  |  |||  || |||||||| |  ||||| |||
Db   746  GGAAAGTGTGGCGGTTCCGGTTACTCGGTTACAGCAGCAGTCAAAGTTACGTGTTGACCA  805

Qy   855  AAGGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTGGTGGTCGGTTAGTTTCA  914
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Db   806  AGGGCTGGAGCCGGTTCGTTCGTTAAAGAAGAATCTTCGAGCCGGTGATGGTGGTTGTTCG  865

Qy   915  GTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAG  974
          || | |  |||| | | | ||||| || | ||| | | ||| ||   |||  || ||||
Db   866  AGAGATCAACGGACCAGACCACCGGCAATTGTATATCCACTGGAAAGTCCCGGTCTAGTCCCGG  925

Qy   975  ATTTAGATCGCGGTCGGGTTTGAGATTGTTCGGAGTTGTTCACCGGAGAGTTCAA  1034
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Db   926  TTCAGACTGTGGTAGGCTATTCCGAGTCATTCATGTGAGTAACGAGAAACCAA  985

Qy  1035  GAAACGACGTCGTA-------GGAAACAAAGAGTGAACGATACTGAGATGTTATCGT  1085
          |||| | |  | ||         ||  | |||  |  | ||   | | ||  || |||
Db   986  ACGACGTCCGACAGTAGAGTGTGTTGGCAAGAGAGATCTCCGGGAAGATGATTTGTTTTCGT  1045

Qy  1086  TGGTGTGTAGCAAGAAGCAACGCATCTTTCACGGCCTCGTAACAACTCTTTCTCTTTTTT  1145
          | ||||||| ||| |  | |||||| || ||||| | | | ||| |  | ||  |||||||
Db  1046  TAGGGTGTTCCAAGAAGCACAGCAGCGGATTATCAACATCTTGTGACAAATTCTTTTTTTTGGT  1105

Qy  1146  TTTCTTT  1152
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Db  1106  TTTTTTT  1112
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CDS              /gene="F14K14.1"
                 2580..2996
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                 /protein_id="AAG52032.1"
                 /db_xref="GI:12324131"
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                 NERKRRRKVSNRESAARSRMRKQRHMEELWSMLVQLINKNKSLVDELSQARECYEKVI
                 BENMKLRBENSKSRKMIGEIGLNRFLSVEADQIWTF"

gene             complement(7929..8372)
                 /gene="F14K14.2"
mRNA             /note="predicted by genefinder"
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                 /gene="F14K14.2"
CDS              complement(7929..8372)
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                 /codon_start=1
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                 /protein_id="AAG52031.1"
                 /db_xref="GI:12324130"
                 /translation="MESPRIHGGAEEKSSCSSGWTMYIEDTFHGNHHSEVVYEEEDDG
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repeat_region    8172..8222
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gene             complement(10880..10953)
                 /gene="60037.tRNA-Ile-1"
tRNA             complement(10880..10953)
                 /gene="60037.tRNA-Ile-1"
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gene             12258..13860
                 /gene="F14K14.4"
                 /note="identical to peroxidase ATP23a GB:CAA70035,
                 GB:Y08782"
mRNA             join(12258,12536,12638..12829,12950..13115,13256..13860)
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CDS              join(12312,12536,12638..12829,12950..13115,13256..13683)
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                 /db_xref="GI:12324132"
                 /translation="MMRLLFVFPMVHTIFIPCFSFDTPGKDLPLTLDYYKSTCPTVFD
                 VIKKEMBCIVKEDPRNAAIIIRLHFHDCFVQGCDGSVLLDETETLQGEKRASPNINSL
                 KGYKIVRIKNIIESECPGVVSCADLLTIGARDATILVGGPNVWGRKDSKTASYE
                 LATTNLPTPEEGLISIIAKFYSQGLSVEBDMVALIGAHTIGKAQCRNFRSRIYGDFQVT
                 SALNPVSETYLASLREICPASSGEGDSNVTAIDNVTPNLFDNSIYHTLLRGEBGLLNSD
                 QEMYTSLFGIQTRRIVSKYAEDPVAFFEQFSKSMVKMGNILNSESLADGBVRRNCRFV
                 NT"

repeat_region    complement(15498..15517)
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gene             complement(15827..17141)
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                 /note="identical to RAV2 GB:BAA34251, GB:AB013887;
                 (putative DNA-binding protein: PF00847 AP2 domain;
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                 DNA-binding protein: Nucleic Acids Res 1999 Jan
                 15;27(2):470-8)"
mRNA             complement(<15827..>17141)
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CDS              complement(15989..17047)
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                 LSVDANGKRNGSSTTQNDKVLKTREVLFEKAVTPSDVGKLNRLVIPKQHAEKHFPLPS
                 PSPAVIKGVLINPEDVNGKVWRFRYSYWNSSQSYVLTKGWSRFVKEKNLRAGDVTFE
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gene             22015..25032
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                 24174..24587,24673..25032)
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CDS              join(22015..22407,22500..22586,22667..22786,22867..22965,
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                 24174..24587,24673..24834)
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                 /db_xref="GI:12324136"
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                 EGEYVLKKATBYGAVBIWMNERVRRACGNSCADFVYGFLDKSSKKGPEYWLLWKYEGE
                 STLAGLMQSKEFPYNVBTIILGKVQDLPKGLERENKIIQTIMRQLLFALDGLHSTGII
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                 PSAPSAPVAAALSPVLWQMNLPDRFDIYSIGLIFLQMAFPSLRSDSNLIQFNRQLKRC
                 DYDLTAWRKLVEPRASADLRRGFELVDLDGGIGWELLTSMVRYKARQRISAKAALAHP
                 YFDRQGLLALSVMQNLRMQYFRATQQDYSEAANWVIQLMAKNGTEKDGGFTETQLQEL
                 REKEPRKKANAQRNALASALRLQRKLVKTVTETIDEISDGRKTVWNNRWIPREE"

gene             complement(28688..29936)
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                 /note="C-term similar to C-term of apoptosis inhibitor
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mRNA             complement(join(<28688..28766,28868..28947,29038..29118,
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                 /gene="F14K14.7"
CDS              complement(join(28688..28766,28868..28947,29038..29118,
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                 /codon_start=1
                 /product="hypothetical protein; 29936-28688"
                 /protein_id="AAG52039.1"
                 /db_xref="GI:12324138"
                 /translation="MVVRYLDWNRGLVVTADDEHQOSNRICGLQDIGGHVMKIPFVTF
                 QIILFMEVEFTPASAKNIPIIVLFVPLFLLQGAGVLFAMYRIVEKSVLLINSGSGSYG
                 RYPTATSSAREFLGFFQHGARLLGWWSIDEGSREEQARLYSGEATGYNTFSPEVVKKM
                 PKSDLVEBIWRIQAALSEQTDITSYSQOEYBRLQNEKILCRVCFBDPINVVLLPCRHH
                 VLCSTCCEKCKKCPICRVLIIERRMPYYDV"

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gene             complement(34606..36199)
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Best Local Similarity  62.7%;    Pred. No. 1e-72;
Matches  741;    Conservative    0;    Mismatches  396;    Indels  44;    Gaps    8;

Qy     43 ATTTCTGTTTCTCCATTGTTCAAACCATARAAAAA--AACACAGATTAAATGGAATCG  100
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Db  17098 ATTTTTGTTTCTTGGTTTGGTGAGAATCTTCAAGAAACTGAAACAAAGAAAATGGATTCT 17039

Qy    101 AGTAGCGTTGATGAG---AGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGGC---- 153
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Db  17038 AGTTGCATAGACGAGATAAGTTCCTCCACTTCAGAATCTTTCTCCGCACCACCGCCAAG 16979

Qy    154 --GATAACTCCGGCGAAAAAGTCTGCTGGTAGGTAACTTATACAGGATGGAAGCGGATCA 211
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Db  16978 AAGCTCTCTTCCTCCTCCGCGGCGGCGGCGTTACGCCTTACGCCTTACCGGATGGGAGCGGGGGGAGC 16919
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us-10-632-436a-1.rge

Tue Sep 13 10:10:51 2005

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ACCESSION   AC011665
VERSION     AC011665.8  GI:12323207
KEYWORDS    HTG.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
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            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 100515)
  AUTHORS   Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
            Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
            Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
  TITLE     Arabidopsis thaliana chromosome 1 BAC T6L1 genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 100515)
  AUTHORS   Lin,X. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-OCT-1999) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
REFERENCE   3  (bases 1 to 100515)
  AUTHORS   Town,C.D. and Kaul,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-2001) The Institute for Genomic Research, 9712
            Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
            On Jan 19, 2001 this sequence version replaced gi:12280894.
            Address all correspondence to:at@tigr.org
COMMENT     BAC clone T6L1 is from Arabidopsis thaliana chromosome 1
            The orientation of the sequence is from SP6 to T7 end of the BAC
            clone.
            Genes were identified by a combination of several methods: Gene
            prediction programs including Genscan+ (Chris Burge,
            http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
            http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
            of GlimmerM, see Mihaela Pertea,
            http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and
            GeneSplicer (Mihaela Pertea and Steven Salzberg, contact
            mpertea@tigr.org), searches of the complete sequence against a
            peptide database and the plant EST database at TIGR
            (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to
            indicate the level of evidence for their annotation. Genes with
            similarity to other proteins are named after the database hits.
            Genes without significant peptide similarity but with EST
            similarity are named as unknown proteins. Genes without protein
            or EST similarity, that are predicted by more than two gene
            prediction programs over most of their length are annotated as
            hypothetical proteins. Genes encoding tRNAs are predicted by
            tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/).
            Simple repeats are identified by repeatmasker (Arian Smit,
            http://ftp.genome.washington.edu/RM/RepeatMasker.html).
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     /chromosome="1"
                     /clone="T6L1"
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                     /rpt_family="(TA)n"
     repeat_region   complement(1046..1089)
                     /rpt_family="AT_rich"
     repeat_region   1501..1592
     repeat_region   complement(1833..1879)
                     /rpt_family="(CAT)n"
     gene            2929..4522
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                     /note="Pfam HMM hit: helix-loop-helix DNA-binding domain"
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Db  16918 AGGGTCGTGTTGGATCCCGAGAACGCGCTAGAGACGACGCCGAAAGCTACCATCTTCA 16859

Qy    272 AAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAGAAA 331
              ||||| ||||||||||||| |||||||| |||||||||||||| |||||||||||||
Db  16858 AAATACAAAGGTGTGTTCCTCAGCCTAACGGAAGATCGGAGCTCAGATCTACGAGAAG 16799

Qy    332 CACCAGGGCGTGGTGGCTCGGACATTCAACGAAGAAGACGAAGCCGCGTCGTGCCTACGAC 391
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Db  16798 CACCAACGAGTATGGCTCGGGACTTTCAAGCAACGAGCAAGAAGAAGCTGTCTGCTCCTACGAC 16739

Qy    392 GTCGCGGTTCACAGGTTCCGTCGCCGTCACGCCCGTCACCAAATTCAAAGACGTGAAGATG 451
              ||| ||||||||| |||||||| || ||||||||||||||||||||||| |||||||
Db  16738 ATCGCAGCTTGTAGATTCCGTGACGCCGACGCCGTCGTCAACTTCAAGAACGT---TCTG 16682

Qy    452 GACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCTGTTGATATGTTG 511
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Db  16681 GAAGACGCGGCGATTTAGCTTTTCTTGAAGCTCACTCAAAGGCCCAGAGATCGTCGACATGTTG 16622

Qy    512 AGGAAAACATACTTATAACGAAGAGTTAGAGCAGCAGAGTAAAACGGCCGTCGTAATGGTAACCGA 571
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Db  16621 AGAAAAACACACTTACGCCGACGAGCTTGAACACAGAACAATAAACGGACAGTTGTTTCTCTCC 16562

Qy    572 AACATGACTAGGACGTTGTTAACCTCGGGTTGAGTAATGATGGTGTTTCTACGACGCGGG 631
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Db  16561 GTCGACGCTAACGGAAAACGTAACGGATCGAGTACTACTCAAAACG------ACAAAGTT 16508

Qy    632 TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAGCTA 691
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Db  16507 TTAAAGACGCGTGAAGTTCTTTTCGAGAGAGGCTGTTACACCTACGCCGACGTTGGGAAGCTA 16448

Qy    692 AACCGTTTGGTTATACGCGAAAATCACCGCAGAGAAACATTTCCGTTACCGTCAAGTAAC 751
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Db  16447 AACCGTCTCGTGATACCTAAACAACACGCCCGAGAAAACACTTTCCGTTACCGTCACCGTCA 16388

Qy    752 GTTTCCGTG---AAAGGAGTGTTGTTGAACTTTGAACGTTAACGGGAAAGTGTGGAGG 808
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Db  16387 CCGGCAGTGACTAAAGGAGTTTTGATCATCCGAAGACGTTAACGTGAAAGTGTGGAGG 16328

Qy    809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
              ||||||||| || |||||| |||| ||| ||||||||||| || |||||||||||||||
Db  16327 TTCCGTTACTCATACTGGAACAGTAGTCAGACAGTAGTTACGTGTTGACCAAGGGATGGAGTCCA 16268

Qy    869 TTCGTTAAGGAGAGAAATCTACGTGCTGGTCGGTGACGTGGTTAGTTCAGTAGATGATCTAACCGT 928
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Db  16267 TTCGTCAAGGAGAAGAATCTTCGAGCCGTGATGTTGTTACTTTCGAGAGATCGACCGGA 16208

Qy    929 CAGGATCAACAGTTGTACATTGGGTGGAA----------GTCGAGATCGCGGGTCAGAT 976
              |||||||||   ||  |||| ||||||||          |||| || ||| ||||||||
Db  16207 CTGAGCGGCAGTTGTATATTGATTGGAAAGTTCGGTCGTCCGGAGAAAAACCCGGTT 16148

Qy    977 TTAGATGCGGGTCGGGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGA 1036
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Db  16147 CAGGTGGTGGTCGTTCCGGCTTTTCGGAGTTGATATCTTTAATGCGACCACCGTGAAGCCAAAC 16088

Qy   1037 AACGACGT-------CGTAGGAACAAAAGAGTGAACCATACTGAGATGTTATCGTTG 1087
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Db  16087 GACGTCGTGCGCCGTTGCGGTGCGAAAGAGATCTCGAGATGTTGATGATATGTTGCGTTA 16028

Qy   1088 GTGTGTAGCAAGAGCAACAGCCATCTTCACGCCCTGTAACAACTCTTCTTTTTTTT 1147
              |||||| ||| || || ||| | ||||||  ||||||| ||||||||||||||||
Db  16027 CGGTGTTCCAAGAAGCAGGCGGATAATCAATGCATATTTCCTTTTGTGACATATTTCCGATTTT 15968

Qy   1148 TCTTTTGTTGTTTAATAATTTTTAAAAACTCCATTTTCGT 1188
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Db  15967 ATGCTTTCGTTTTTTAATTTTTTTTTTTTGTCAAGTTGTGT 15927
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RESULT 15
AC011665
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DEFINITION Arabidopsis thaliana chromosome 1 BAC T6L1 genomic sequence,

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gene            21988..23302
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mRNA            21988..23302
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                LSVDANGKRNGSSTTQNDKVLKTREVLFEKAVTPSDVGKLNRLVIPKQHAEKHFPLPS
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                GB:P23970 (Bacillus subtilis); Pfam HMM hit:
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Best Local Similarity  62.7%;  Pred. No. 1e-72;
Matches  741;  Conservative   0;  Mismatches  396;  Indels  44;  Gaps   8;

Qy        43 ATTTCTGTTCTCCCATTGTTCAAACCATAAAAAAA--AACACAGATTAAATGGAATCG 100
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Db     22031 ATTTTTGTTTCTTGGTTTGGTGAGAATCTTCAAGAAACTGAAACAAAGAAAATGGAATCCT 22090

Qy       101 AGTAGCGTTGATGAG---AGTACTACAAGTACAGGTTCCATCTGTGAAACCCCCGGC---- 153
             |||||||||||||||   ||||||||||||||||||||| |||||||||| || |||
Db     22091 AGTTGCATAGACGAGATAAGTTCCACTTCCAGAATCTTTCTCCCGCACCACCGCCAAG 22150

Qy       154 --GATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA 211
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Db     22151 AAGCTCTCTCCTCGCCGCGCGGTTACGCCTCTACCGGATGGGAAGCGGCGGGAGC 22210

Qy       212 AGGCGTTGTTAGATTCAGAGAACGACGGCCTAGAAGCTGAAGCTGAATCTGAAGGTCGTCA 271
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Db     22211 AGGCTCGTCGTGTTGGATCCCGAGAACGGCCTCAGCACGACGCGGAGCTACCAATCTTCA 22270
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Qy    272  AAATACAAAGGTGTGTGCCACAACCAAAACGGAAGATGGGAGCTCAGATTTACGAGAAA    331
           |||||||||||| || ||| |||||||||| || ||||||| ||||||||||||||||
Db  22271  AAATACAAAGGTGTTGTTCCTAGCCTAACGGAAGATGGGAGCTCAGATCTACGAGAAG  22330

Qy    332  CACCAGCGCCGTGTGGCTCGGGACATTCAACGAAGAACGAAGCCGCTCGTGCCTACGAC    391
           |||||  ||||| || |||||||| ||||||||||||||||| |||||||| ||||||
Db  22331  CACCAACGAGTATGGCTCCGGACTTTCACGAGCAAGAAGAAGCTGCTCGTCCTTCCTACGAC  22390

Qy    392  GTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAGATG    451
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Qy    452  GACGAAGACGAGGTCGATTTCTTGAATTCATTCGAAATCTGAGATCGTTGATATGTTG    511
           || |  ||| |  ||||| | |||  ||||||| |||||||| ||||||| |||||||
Db  22448  GAAGACGGCGATTTAGCTTTCTTGAAGCTCACTCAAAGGCCGAGATCGTCGACATGTTG  22507

Qy    512  AGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGA    571
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Db  22508  AGAAAACACACTTACGCCGACGAGCTTGAACAGACAGAACAATAAACGGCAGTTGTTTCTCTCC  22567

Qy    572  AACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGG    631
                 |||| |||    || || |||| |||  ||||| || |||||| ||||||| ||
Db  22568  GTCACGCTAACGGAAAACGTAACGGATCGAGTACTACTCAAAACG-----ACAAAGTT  22621

Qy    632  TTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTA    691
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Qy    692  AACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAAC    751
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Qy    752  GTTTCCGTG---AAAGGAGTGTGTTGAACTTGGAGGACGTTAACGGAAAGTGTGGAGG    808
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Db  22742  CCGGCAGTGACTAAAGGAGTTTTGATCAACTTCAAGACGTTAACGGTAAAGTGTGGAGG  22801

Qy    809  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG    868
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Qy    869  TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT    928
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Qy    929  CAGGATCAACAGTTGTACATTGGGTGGAA-----------GTCGAGATCCGGGTCAGAT    976
           || || ||| |||    ||| ||||| ||           || ||||||||||||| |
Db  22922  CTAGAGCGGCAGTTATATATTGATTGGAGAAAGTTCGGTCGTCTGGTCCGAGAGAAAACCCGGTT  22981

Qy    977  TTAGATGCGGGTCGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGA    1036
           || || |||  || ||||| ||| ||    ||||   || |||    |||||| |||
Db  22982  CAGGTGGTGGTTGGCTTTTCGGCTTTTCGGAGTTGATATCTTTAATGTGACCACCGTGAAGCCAAAC  23041

Qy   1037  AACGACGT-------CGTAGGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTG    1087
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Qy   1088  GTGTGTAGCAAGAAGCAACGCCATCTTCACGCCTCGTAACAACTCCTCTCTCTTTTTTT    1147
           |||||| |||| ||    ||| ||  |||  || |||  |||  |||||||||| |||||
Db  23102  CGGTGTTCCAAGAAGCAGCGGCGATAATCAAGGCTTTGTGACATAATTCCTTTTCCGATTTT  23161

Qy   1148  TCTTTTGTTGTTTAATAATTTTTAAAAACTCCATTTTCGT  1188
           | ||| || || ||  |   ||||||| ||| |||||| |
Db  23162  ATGCTTTCGTTTTGTTTTAATTTTTTTTTTTTTGTCAAGTTGTGT  23202
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Search completed: September 11, 2005, 02:50:38
Job time : 6003.04 secs

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OM nucleic - nucleic search, using sw model

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          GenCore version 5.1.6
     Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: September 10, 2005, 20:12:16 ; Search time 799.949 Seconds
                         (without alignments)
                    9679.392 Million cell updates/sec

Title: US-10-632-436A-1
Perfect score: 1308
Sequence: 1 gatacatatacacaacata.......ttaaaaagggtacttagat 1308
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
          1: geneseqm1980s:*
          2: geneseqm1990s:*
          3: geneseqm2000s:*
          4: geneseqm2001as:*
          5: geneseqm2001bs:*
          6: geneseqm2002as:*
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          9: geneseqm2003bs:*
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         11: geneseqm2003ds:*
         12: geneseqm2004as:*
         13: geneseqm2004bs:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Match Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1308 | 100.0 | 1308 | 12 | ADM13467 | Adm13467 Arabidops |
| 2 | 1308 | 100.0 | 3835 | 10 | ABT16588 | Abt16588 Ethylene |
| 3 | 1255 | 95.9 | 1281 | 4 | AAD05842 | Aad05842 Arabidops |
| 4 | 1255 | 95.9 | 1281 | 5 | AAD06649 | Aad06649 A. thalia |
| 5 | 1255 | 95.9 | 1281 | 6 | ABK65156 | Abk65156 Arabidops |
| 6 | 1255 | 95.9 | 1281 | 9 | ADA15448 | Ada15448 DNA encod |
| 7 | 1255 | 95.9 | 1281 | 9 | ACD98391 | Acd98391 A. thalia |
| 8 | 1255 | 95.9 | 1281 | 10 | ADB31784 | Adb31784 DNA encod |
| 9 | 1255 | 95.9 | 1281 | 10 | ADD55665 | Add55665 Thalecres |
| 10 | 1255 | 95.9 | 1281 | 10 | ADD30762 | Add30762 Plant yie |
| 11 | 1255 | 95.9 | 1281 | 10 | ADB37198 | Ade37198 Plant yie |
| 12 | 1255 | 95.9 | 1281 | 10 | AAD47502 | Aad47502 Arabidops |
| 13 | 1255 | 95.9 | 1281 | 12 | ADI41706 | Adi41706 Plant tra |
| 14 | 1255 | 95.9 | 1281 | 12 | ADO02166 | Ado02166 Thalecres |
| 15 | 1255 | 95.9 | 1281 | 12 | ADP67768 | Adp67768 Arabidops |
| 16 | 1035 | 79.1 | 1035 | 6 | ABZ14511 | Abz14511 Arabidops |
| c 17 | 971.8 | 74.3 | 1003 | 6 | ABN98461 | Abn98461 Arabidops |
| 18 | 527.4 | 40.3 | 573 | 3 | AAC32867 | Aac32867 Arabidops |
| 19 | 517.8 | 39.6 | 1155 | 4 | AAD05843 | Aad05843 Arabidops |
| 20 | 517.8 | 39.6 | 1155 | 5 | AAD06665 | Aad06665 A. thalia |
| 21 | 517.8 | 39.6 | 1155 | 6 | ABK65166 | Abk65166 Arabidops |
| 22 | 517.8 | 39.6 | 1155 | 10 | ADD30387 | Add30387 Plant yie |
| 23 | 517.8 | 39.6 | 1155 | 10 | ADE37138 | Ade37138 Plant yie |
| 24 | 517.8 | 39.6 | 1155 | 10 | ADE31464 | Ade31464 Plant yie |
| 25 | 517.8 | 39.6 | 1155 | 12 | ADI41906 | Adi41906 Plant tra |
| 26 | 517.8 | 39.6 | 1155 | 12 | ADO03478 | Ado03478 Thalecres |
| 27 | 517.8 | 39.6 | 1155 | 12 | ADP67774 | Adp67774 Arabidops |
| 28 | 517.8 | 39.6 | 1235 | 3 | AAC50721 | Aac50721 Arabidops |
| 29 | 517.8 | 39.6 | 1244 | 3 | AAC40426 | Aac40426 Arabidops |
| c 30 | 517.8 | 39.6 | 3802 | 10 | ABT16587 | Abt16587 Ethylene |
| 31 | 493.8 | 37.8 | 969 | 12 | ADP67808 | Adp67808 Cauliflow |
| 32 | 394.2 | 30.1 | 1262 | 3 | AAC39864 | Aac39864 Arabidops |
| 33 | 391.2 | 29.9 | 3886 | 10 | ABT16585 | Abt16585 Ethylene |
| 34 | 389.8 | 29.8 | 1239 | 4 | AAD05841 | Aad05841 Arabidops |
| 35 | 389.8 | 29.8 | 1239 | 5 | AAD06667 | Aad06667 A. thalia |
| 36 | 389.8 | 29.8 | 1239 | 6 | ABK65329 | Abk65329 Arabidops |
| 37 | 389.8 | 29.8 | 1239 | 9 | ADA15450 | Ada15450 DNA encod |
| 38 | 389.8 | 29.8 | 1239 | 10 | ADB31802 | Adb31802 DNA encod |
| 39 | 389.8 | 29.8 | 1239 | 10 | ADD30545 | Add30545 Plant yie |
| 40 | 389.8 | 29.8 | 1239 | 10 | AAD47491 | Aad47491 Thalecres |
| 41 | 389.8 | 29.8 | 1239 | 12 | ADO03414 | Ado03414 Thalecres |
| 42 | 389.8 | 29.8 | 1239 | 12 | ADP67772 | Adp67772 Arabidops |
| 43 | 389.8 | 29.8 | 1239 | 13 | ADI43608 | Adi43608 Plant tra |
| 44 | 379.4 | 29.0 | 3859 | 10 | ABT16586 | Abt16586 Ethylene |
| 45 | 378.4 | 28.9 | 1246 | 4 | AAD05827 | Aad05827 Arabidops |

ALIGNMENTS

```
RESULT 1
ADM13467
ID   ADM13467 standard; cDNA; 1308 BP.
XX
AC   ADM13467;
XX
DT   15-JUL-2004  (first entry)
DE   Arabidopsis AP2 domain transcription factor RAV1 cDNA.
XX
KW   plant growth regulant; chimeric plant-expressible gene; plant;
KW   mRNA transcription; freezing tolerance; drought tolerance;
KW   transcription regulating protein; binding protein; AP2 domain;
KW   cold regulatory gene; dehydration regulatory gene; RAV1 gene; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   US2004078852-A1.
XX
PD   22-APR-2004.
XX
PF   01-AUG-2003; 2003US-00632436.
XX
PR   02-AUG-2002; 2002US-0400777P.
XX
PA   (THOM/) THOMASHOW M F.
PA   (FOWL/) FOWLER S G.
PA   (VOGE/) VOGEL J.
PA   (ZARK/) ZARKA D.
XX
PI   Thomashow MF, Fowler SG, Vogel J, Zarka D;
XX
DR   WPI; 2004-340088/31.
XX
PT   Chimeric plant expressible gene encoding a cold-regulated transcription
PT   factor ( ZAT12 or RAV1), is useful in inducing freezing or drought
PT   tolerance in a plant.
XX
PS   Claim 3; SEQ ID NO 1; 52pp; English.
XX
CC   The invention describes a chimeric plant-expressible gene comprising in
CC   the 5' to 3' direction: (a) a promoter capable of effecting mRNA
CC   transcription in the selected plant cell to be transformed, operably
```

CC   linked to (b) a structural DNA sequence encoding the 1308bp sequence
CC   (SEQ. ID. No. 1) or 816bp (SEQ. ID. 2) that induces freezing or drought
CC   tolerance, operably linked to (c) a non-translated region of a gene
CC   encoding a signal sequence for polyadenylation of mRNA. Also described
CC   are: plant material transformed with DNA comprising fully defined
CC   sequences of 1308 or 816 bp and encoding a transcription regulating
CC   protein or binding protein comprising an AP2 domain amino acid sequence;
CC   a plant tissue comprising plant cells susceptible to infection with
CC   Agrobacterium tumefaciens that contain and express the chimeric gene; and
CC   a method for regulating cold and dehydration regulatory genes in a plant.
CC   The materials are useful in regulating cold and dehydration regulatory
CC   genes in a plant to induce freezing and drought tolerance. This sequence
CC   represents a polynucleotide encoding the putative AP2 domain
CC   transcription factor RAV1 that can be used in the creation of the
XX   chimeric plant-expressible gene of the invention.
XX
SQ   Sequence 1308 BP; 381 A; 226 C; 331 G; 370 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1308; DB 12; Length 1308;
Best Local Similarity 100.0%;   Pred. No. 1e-300;
Matches 1308;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 GTATACATATACACACACATAATTCACAACACAACAACACAAACACATTTCGTTTTCTCCATT   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GTATACATATACACACACATAATTCACAACACAACAACACAAACACATTTCGTTTTCTCCATT   60

Qy   61 GTTTCAAACCATAAAAAAAACACAGATTAAATGAAATCGAGTAGCGTTGATGAGAGTAC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTTTCAAACCATAAAAAAAACACAGATTAAATGAAATCGAGTAGCGTTGATGAGAGTAC 120

Qy   121 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 180

Qy   181 AGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTAGATTCAGAGAACGCGT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTAGATTCAGAGAACGCGT 240

Qy   241 AGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAA 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAA 300

Qy   301 CGGAAGATGGGGAGCTTCAGATTCGTCGATTCAGAGAAACACCAGCGCGTGTGGCTCGGG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CGGAAGATGGGGAGCTTCAGATTCGTCGATTCAGAGAAACACCAGCGCGTGTGGCTCGGG 360

Qy   361 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCCACAGTTCCGTCGCCGTGA 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCCACAGTTCCGTCGCCGTGA 420

Qy   421 CGCCGTCACAAATTTCAAAGACGTGAAGATGACGAAGAAGACGAAGTCGATTTCTTGAATTC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CGCCGTCACAAATTTCAAAGACGTGAAGATGACGAAGAAGACGAAGTCGATTTCTTGAATTC 480

Qy   481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATACGAAGAAGAGTTAGA 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATACGAAGAAGAGTTAGA 540

Qy   541 GCAGAGTAAACGGCGTCGTAATGGTAACGGAACATGACTAGGACGTTGTTAACGTCGGG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GCAGAGTAAACGGCGTCGTAATGGTAACGGAACATGACTAGGACGTTGTTAACGTCGGG 600

Qy   601 GTTGAGTAATGATGGTGTTTCTACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGAA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GTTGAGTAATGATGGTGTTTCTACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGAA 660

Qy   661 AGCGGGTAACGCCAAGCCACGTTGGGAAGCTAAACCGTTGGTTATACCGAAACATCACGC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AGCGGGTAACGCCAAGCCACGTTGGGAAGCTAAACCGTTGGTTATACCGAAACATCACGC 720

Qy   721 AGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTT 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTT 780

Qy   781 TGAGGACGTTAACGGAAAGTGTGGAGGTTCGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGAGGACGTTAACGGAAAGTGTGGAGGTTCGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG 840

Qy   841 TTATGTTTGACTAAAGGTTGGAGCAGTTCGTTAAGGAGAGAAATCTACGTTGCTGGTGA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTATGTTTGACTAAAGGTTGGAGCAGTTCGTTAAGGAGAGAAATCTACGTTGCTGGTGA 900

Qy   901 CGTGGTAGTTTCAGTAGATCTAACGGTCAGGATCACACAGTTGTACATTGGGTGGAAGTC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CGTGGTAGTTTCAGTAGATCTAACGGTCAGGATCACACAGTTGTACATTGGGTGGAAGTC 960

Qy   961 GAGATCCGGGTCAGATTTAGATGCGGGTCGGGTTCGGGTTTGAGATTGTTCGGAGTTAACATTC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GAGATCCGGGTCAGATTTAGATGCGGGTCGGGTTCGGGTTTGAGATTGTTCGGAGTTAACATTC 1020

Qy   1021 ACCGGAGAGTTCAAGAAACGACGTCGTAGGAAGAAACAAAAGAGTGAACGATACTGAGATGTT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACCGGAGAGTTCAAGAAACGACGTCGTAGGAAGAAACAAAAGAGTGAACGATACTGAGATGTT 1080

Qy   1081 ATCGTTGGTGTGTAGCAAGAAGAGCAACGGCATCTTCACGCCTCGTAACACTCTTCTCTT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCGTTGGTGTGTAGCAAGAAGAGCAACGGCATCTTCACGCCTCGTAACACTCTTCTCTT 1140

Qy   1141 TTTTTTTCTTTTTGTTGTTTTAATAATTTTTAAAAACTCCATTTTCGTTTTCTTTATTG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TTTTTTTCTTTTTGTTGTTTTAATAATTTTTAAAAACTCCATTTTCGTTTTCTTTATTG 1200

Qy   1201 CATCGGTTCTTCTTCTTCTTCTGTTCACCAAAGGTTCATGAGTTGTTTTGTTTGTATTGATGA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CATCGGTTCTTCTTCTTCTTCTGTTCACCAAAGGTTCATGAGTTGTTTTGTTTGTATTGATGA 1260

Qy   1261 ACTGTAAATTTATTTATAGGATAAATTTAAAAGGGTTACTTAGAT 1308
             |||||||||||||||||||||||||||||||||||||||||||||
Db   1261 ACTGTAAATTTATTTATAGGATAAATTTAAAAGGGTTACTTAGAT 1308

RESULT 2
ABT16588
ID   ABT16588 standard; DNA; 3835 BP.
XX
AC   ABT16588;
XX
DT   03-APR-2003 (first entry)
XX
DE   Ethylene insensitivity related mouse-ear cress DNA SEQ ID No 62.
XX
KW   Mutant; transformed plant; ethylene-response DNA-binding factor; edf1;
KW   edf2; edf3; edf4; fruit; transgenic plant; floral industry;
KW   fruit processing industry; floral senescence; flower longevity;
KW   decreased floral initiation; post-harvest; transportation;
KW   mouse-ear cress; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200289555-A2.
XX
PD   14-NOV-2002.
XX
PF   08-MAY-2002; 2002WO-US014592.
XX
PR   08-MAY-2001; 2001US-0289364P.
PR   08-MAY-2001; 2001US-0289835P.
XX
PA   (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI   Stepanova AN, Ecker JR;
XX
DR   WPI; 2003-120491/11.
XX
PT   Novel mutant or transformed plant comprising mutated forms of edf1, edf2,
PT   edf3 and edf4 genes, and having decreased ethylene sensitivity, such that

PT   its fruit ripens more slowly than wild-type version of the plant.
XX
PS   Disclosure; Page 80-81; 85pp; English.
XX
CC   The invention relates to a mutant or transformed plant comprising mutated
CC   forms of ethylene-response DNA-binding factors (edf1, edf2, edf3 and
CC   edf4 genes such that the plant exhibits a decreased response to ethylene,
CC   and comprises fruit which ripens more slowly than a wild-type version of
CC   the plant. The transgenic plants having reduced sensitivity to ethylene
CC   are useful for floral industry and fruit processing industries. Since
CC   ethylene is involved in floral senescence, the modified plants have
CC   longer flower longevity. The modified plants e.g. lettuce, spinach, other
CC   leafy vegetables provide higher yields due to decreased floral
CC   initiation, since the transformed plants do not bolt or flower easily.
CC   The plants provide fruits which ripens more slowly than the wild-type
CC   version of the plant, and thus are advantageous in post-harvest and
CC   transportation conditions. This polynucleotide represents the DNA of a
CC   mouse-ear cress sequence used in the ethylene sensitivity modulation
CC   process of the invention
XX
SQ   Sequence 3835 BP; 1310 A; 662 C; 677 G; 1186 T; 0 U; 0 Other;

Query Match   100.0%;   Score 1308; DB 10;   Length 3835;
Best Local Similarity 100.0%;   Pred. No. 1.4e-300;
Matches 1308; Conservative   0; Mismatches   0; Indels   0;   Gaps   0;

Qy   1 GTATACATATACACAACAACATAATTCACAACAACAACACAACACATTTCTGTTTTCTCCATT   60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2410 GTATACATATACACAACAACATAATTCACAACAACAACACAACACATTTCTGTTTTCTCCATT 2469

Qy   61 GTTTCAAACCATAAAAAAAACACAGATTAAATGGAATCGAGTAGCGTTGATGAGAGTAC   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2470 GTTTCAAACCATAAAAAAAACACAGATTAAATGGAATCGAGTAGCGTTGATGAGAGTAC 2529

Qy   121 TACAAGTACAGGTTCCATCTGTGAAACCCGGCGATAACTCCCGGCGAAAAGTCGTCGGT   180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2530 TACAAGTACAGGTTCCATCTGTGAAACCCGGCGATAACTCCCGGCGAAAAGTCGTCGGT 2589

Qy   181 AGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGGCT   240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2590 AGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGGCT 2649

Qy   241 AGAAGCTGAATCTAGGAGAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAA   300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2650 AGAAGCTGAATCTAGGAGAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAA 2709

Qy   301 CGGAAGATGGGGAGCTCAGATTTACGAGAAAACACCAGCGGCGTGGGCTTCGGGACATTCAA   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2710 CGGAAGATGGGGAGCTCAGATTTACGAGAAAACACCAGCGGCGTGGGCTTCGGGACATTCAA 2769

Qy   361 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCCATCAGAGGTTCCGTCGTCGTCCGTGTGA   420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2770 CGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCCATCAGAGGTTCCGTCGTCGTCCGTGTGA 2829

Qy   421 CGCCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTC   480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2830 CGCCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTC 2889

Qy   481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAAACATACTTATAACGAAGAGTTAGA   540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2890 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAAACATACTTATAACGAAGAGTTAGA 2949

Qy   541 GCAGAGTAAACGGCGTCGTAATGGTAACGGAACATGACTAGGACGTTGTTAACGTCGGG   600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2950 GCAGAGTAAACGGCGTCGTAATGGTAACGGAACATGACTAGGACGTTGTTAACGTCGGG 3009

Qy   601 GTTGTAGTAATGATGGTGTTCTCACGACGGGGTTTAGATCGGCGGACACTGTTTGAGAA   660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3010 GTTGTAGTAATGATGGTGTTCTACGACGGGGTTTAGATCGGCGGACACTGTTTGAGAA 3069

Qy   661 AGCGGTAAACGGACGCGTTGGGAAGCTAAACCGTTTGTTTATACCGAAACATCACGC   720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3070 AGCGGTAAACGGACGCGTTGGGAAGCTAAACCGTTTGTTTATACCGAAACATCACGC 3129

Qy   721 AGAGAAACATTTCCGTTACCGTCAAGTAACGTTCCGTCAAGTAACGTTCCGTGAAAGGAGTCGTTGTTGAACTT   780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3130 AGAGAAACATTTCCGTTACCGTCAAGTAACGTTCCGTCAAGTAACGTTCCGTGAAAGGAGTGTTGTTGAACTT 3189

Qy   781 TGAGGACGTTAACGGGAAAGTGTGGAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG   840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3190 TGAGGACGTTAACGGGAAAGTGTGGAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCAGAG 3249

Qy   841 TTATGTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGAGAATCTACGTGCTGGTGA   900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3250 TTATGTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGAGAATCTACGTGCTGGTGA 3309

Qy   901 CGTGGTTAGTTCAGTAGATCTAACGTTCAGGATCAACAGTTGGTACATTGGGTCGGAAGTC   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3310 CGTGGTTAGTTCAGTAGATCTAACGTTCAGGATCAACAGTTGTACATTGGGTCGGAAGTC 3369

Qy   961 GAGATCCGGTCAGATTTAGATCGGGGTTTGAGATTGTTCGGAGTTAACATTTC 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3370 GAGATCCGGTCAGATTTAGATCGGGGTTTGAGATTGTTCGGAGTTAACATTTC 3429

Qy   1021 ACCGGAGAGTTCAAGAAACGACGCTCGTAGGAAACAAAGAGTGAACGATACTGAGATGTT 1080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3430 ACCGGAGAGTTCAAGAAACGACGCTCGTAGGAAACAAAGAGTGAACGATACTGAGATGTT 3489

Qy   1081 ATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTCACGCCTCGTAACAACTCTTCTTCTT 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3490 ATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTCACGCCTCGTAACAACTCTTCTTCTT 3549

Qy   1141 TTTTTTTTCTTTTGTTGTTTAATAATTTTAAAAACTCCATTTCGTTTTCGTTTTCTTATTTG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3550 TTTTTTTTCTTTTGTTGTTTAATAATTTTAAAAACTCCATTTCGTTTTCGTTTTCTTATTTG 3609

Qy   1201 CATCGGTTCTTCTTCTGTTTACCAAAGGTTCATGAGTTGTTTTGTGTATTGATGA 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3610 CATCGGTTCTTCTTCTGTTTACCAAAGGTTCATGAGTTGTTTTGTGTATTGATGA 3669

Qy   1261 ACTGTAAATTTATTTATAGGATAAATTTTAAAAAGGGTTACTTAGAT 1308
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   3670 ACTGTAAATTTATTTATAGGATAAATTTTAAAAAGGGTTACTTAGAT 3717

RESULT 3
AAD05842
ID   AAD05842 standard; cDNA; 1281 BP.
XX
AC   AAD05842;
XX
DT   31-JUL-2001 (first entry)
XX
DE   Arabidopsis thaliana transcription factor G867 cDNA.
XX
KW   Transcription factor; trait modification; structural characteristic;
KW   developmental characteristic; gene therapy; agricultural biotechnology;
KW   ss.
XX
OS   Arabidopsis thaliana.
XX
FH   Key   Location/Qualifiers
FT   CDS   64..1098
FT   /*tag= a
FT   /product= "Transcription factor G867"
XX
PN   WO200136444-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-US031325.
XX
PR   17-NOV-1999; 99US-0166228P.
PR   17-APR-2000; 2000US-0197899P.
PR   22-AUG-2000; 2000US-0227439P.
XX

```
PA   (MEND-)  MENDEL BIOTECHNOLOGY INC.
PA   (RIEC/)  RIECHMANN J L.
PA   (REUB/)  REUBER L.
PA   (KEDD/)  KEDDIE J.
PA   (RATC/)  RATCLIFFE O.
PA   (HEAR/)  HEARD J.
PA   (SAMA/)  SAMAHA R.
PA   (YUGG/)  YU G.
PA   (JIAN/)  JIANG C.
XX
PI   Riechmann JL, Reuber L, Keddie J, Ratcliffe O, Heard J, Samaha R;
PI   Yu G, Jiang C;
XX
DR   WPI; 2001-335996/35.
DR   P-PSDB; AAE01964.
XX
PT   Nucleic acids encoding plant transcription factor polypeptides, useful
PT   for altering the developmental and structural characteristics of plants,
PT   e.g. corn, potato and cotton plants.
XX
PS   Claim 4; Page 111-113; 140pp; English.
XX
CC   The present sequence is Arabidopsis thaliana transcription factor G867
CC   cDNA. This sequence is homologous to transcription factor G9. The
CC   transcription factors are used to modify traits associated with
CC   structural or developmental characteristics of plants, e.g. soybean,
CC   wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa,
CC   sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry,
CC   cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes,
CC   honey dew, lettuce, mango, melon, papaya, peas, watermelon, pineapple,
CC   spinach, squash, sweet corn, tobacco, tomato, peppers, onion, rosaceous
CC   fruits and/or vegetable brassicas when their expression levels are
CC   altered. The manipulation of transcription factor levels in plants offers
CC   great potential in agricultural biotechnology for modifying plant's
CC   traits. The transcription factors are also used in gene therapy;
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match         95.9%;  Score 1255;  DB 4;  Length 1281;
Best Local Similarity   99.9%;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;
```

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Qy      29 CACACACAAACACATTCTGTTGTTCCCATTGTTCAAACCATAAAAAAAAAAACACAGAT 88
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CACACACAAACACATTCTGTTGTTCCCATTGTTCAAACCATAAAAAAAAAAACACAGAT 60

Qy      89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACACAAGTACAGGTACAGTACGAAACC 148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACACAAGTACAGGTACAGTACGAAACC 120

Qy     149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy     209 TCAAGCCGTTGTGTTGTAGATTCAGAGAACGGCGTAGAAGCGGCGTAGAAGCTTCCGTCG 268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCAAGCCGTTGTGTTGTAGATTCAGAGAACGGCGTAGAAGCGGCGTAGAAGCTTCCGTCG 240

Qy     269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAAGCTCAGATTTACGAG 328
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAAGCTCAGATTTACGAG 300

Qy     329 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGAACGAAGCCGCTCGTCGCCTAC 388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGAACGAAGCCGCTCGTCGCCTAC 360

Qy     389 GACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCCGTCACAAATTTCAAAGACGTGAAG 448
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCCGTCACAAATTTCAAAGACGTGAAG 420

Qy     449 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTTCATTCGAAATCTGAGATCGTTGATATG 508
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTTCATTCGAAATCTGAGATCGTTGATATG 480

Qy     509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGTAAACGGCGTCGTAATGGTAAC 568
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGTAAACGGCGTCGTAATGGTAAC 540

Qy     569 GGAAACATGACTAGGACGTTGTTGAGTAATGATGTGTTCTACGACG 628
            ||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGAAACATGACTAGGACGTTGTTGAGTAATGATGTGTTCTACGACG 600

Qy     629 GGGTTAGATCGGCGGAGGCACTGTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGGTTAGATCGGCGGAGGCACTGTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy     689 CTAAACCGTTGTTGTTATACCGGAACATCACCAGAGAAACATTTTCCGTTACCGTCAAGT 748
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTAAACCGTTGTTGTTATACCGGAACATCACCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy     749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGGAAAGTGTGGAGG 808
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGGAAAGTGTGGAGG 780

Qy     809 TTCCGGTTACTCGTATTGGAACAGTAGTCAGAGTATGTTTTGACTAAAGGTTGGAGCAGG 868
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTCCGGTTACTCGTATTGGAACAGTAGTCAGAGTATGTTTTGACTAAAGGTTGGAGCAGG 840

Qy     869 TTCGTTAAGGAGAAGAATCTCACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TTCGTTAAGGAGAAGAATCTCACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy     929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGT 988
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGT 960

Qy     989 CGGGTTTTGAGATTGTTCGGAGTAACATTCACCGGAGAGTTCAAGAACGACGTCGTA 1048
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGGGTTTTGAGATTGTTCGGAGTAACATTCACCGGAGAGTTCAAGAACGACGTCGTA 1020

Qy    1049 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAGCAACGC 1108
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAGCAACGC 1080

Qy    1109 ATCTTTCACGCCTCGTAACAACTCTCTTCTCTTTTCTTTTTGTTTGTTTGTTTTAATAATT 1168
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    1081 ATCTTTCACGCCTCGTAACAACTCTCTTCTC-TTTTTTTCTTTTTGTTTGTTTTAATAATT 1139

Qy    1169 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGTTTCTTTCTTTGTTTACCAA 1228
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGTTTCTTTCTTTGTTTACCAA 1199

Qy    1229 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT 1288
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTATTTATAGGATAAATT 1259

Qy    1289 TTAAAAA 1295
            |||||||
Db    1260 TTAAAAA 1266
```

```
RESULT 4
AAD06649
ID   AAD06649 standard; cDNA; 1281 BP.
XX
AC   AAD06649;
XX
DT   10-AUG-2001 (first entry)
XX
DE   A. thaliana transcription factor G867 cDNA.
XX
KW   Plant transcription factor; phenotype; sugar sensing characteristic;
KW   transgenic plant; plant yield; growth; germination; photosynthesis;
KW   glyoxylate metabolism; respiration; pathogen response; wounding response;
KW   cell cycle regulation; pigmentation; flowering; senescence; physiology;
KW   storage organ; metabolism; ss.
```

```
XX
OS   Arabidopsis thaliana.
XX
FH   Key             Location/Qualifiers
FT   CDS             64..1098
FT                   /*tag= a
FT                   /product= "Transcription factor"
XX
PN   WO200135725-A1.
XX
PD   25-MAY-2001.
XX
PF   14-NOV-2000; 2000WO-US031414.
XX
PR   17-NOV-1999; 99US-0166228P.
PR   17-APR-2000; 2000US-0197899P.
PR   22-AUG-2000; 2000US-0227439P.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
PA   (JIAN/) JIANG C.
PA   (HEAR/) HEARD J.
PA   (PINE/) PINEDA O.
PA   (PILG/) PILGRIM M.
PA   (ADAM/) ADAM L.
PA   (RIEC/) RIECHMANN J L.
PA   (YUGG/) YU G.
PA   (SAMA/) SAMAHA R.
XX
PI   Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
PI   Yu G, Samaha R;
XX
DR   WPI; 2001-335977/35.
DR   P-PSDB; AAE02548.
XX
PT   Nucleic acids encoding plant transcription factor polypeptides, useful
PT   for altering the sugar sensing characteristics of plants and increasing
PT   yield, e.g. corn, potato and cotton plants.
XX
PS   Claim 4; Page 83-84; 151pp; English.
XX
CC   The patent relates to polynucleotides encoding 35 plant transcription
CC   factors which may be used to modify phenotype associated with a plant's
CC   sugar sensing characteristics and increasing yield when their expression
CC   level is altered. Sugars are central regulatory molecules that control
CC   aspects of physiology, metabolism and development. Therefore the cDNAs
CC   and proteins of the invention are useful for modifying the growth and
CC   germination rates of plants, photosynthesis, glyoxylate metabolism,
CC   respiration, starch and sucrose synthesis and degradation, pathogen
CC   response, wounding response, cell cycle regulation, pigmentation,
CC   flowering and senescence of plants and for modifying sink-source
CC   relationships in seeds, tubers, roots, and other storage organs leading
CC   to an increase in yield. The transcription factor polynucleotides and
CC   polypeptides may be used to alter the structure and developmental
CC   characteristics of plants such as soybean, wheat, corn, potato, cotton,
CC   rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,
CC   blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
CC   coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,
CC   onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
CC   tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
CC   The present sequence is an Arabidopsis thaliana transcription factor cDNA
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match             95.9%;  Score 1255;  DB 5;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 4e-288;
Matches  1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps  1;

Qy         29 CACAACACAAACACATTCGTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACACAGAT 88
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 CACAACACAAACACATTTCGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACACAGAT 60

Qy         89 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC 120

Qy        149 CCGGCGATAACTCCGGCGGAAAAGTCGTCGGTAGTAACTTATACAGGAGGAAGCGGA 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGCGATAACTCCGGCGGAAAAGTCGTCGGTAGTAACTTATACAGGAGGAAGCGGA 180

Qy        209 TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGAGAGCTTCCGTCG 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGAGAGCTTCCGTCG 240

Qy        269 TCAAAATACAAAGGTGTGTGCCACAACCAAACCGAAGATGGGAGCTCAGATTTACGAG 328
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAAAATACAAAGGTGTGTGCCACAACCAAACCGAAGATGGGAGCTCAGATTTACGAG 300

Qy        329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAGAAGAAGACGAAGCCGCTCGTGCCTAC 388
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy        389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTCAAAGACGTGAAG 448
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTCAAAGACGTGAAG 420

Qy        449 ATGGACGAAGCAGAGTCGAGTTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 508
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGACGAAGCAGAGTCGAGTTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy        509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGCGTCGTAATGGTAAC 568
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy        569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy        629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCGTAACGCCAAGCGACGTTGGGAAG 688
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCGTAACGCCAAGCGACGTTGGGAAG 660

Qy        689 CTAAACCGTTTGGTTATACCGAGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 748
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTAAACCGTTTGGTTATACCGAGAGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 720

Qy        749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAGG 808
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAAAGTGTGGAGG 780

Qy        809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTAGTGTTTGACTAAAGGTTGGAGCAGG 868
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTAGTGTTTGACTAAAGGTTGGAGCAGG 840

Qy        869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGGTGGTGTTAGTTTCAGTAGATCTAACGGT 928
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGGTGGTGTTAGTTTCAGTAGATCTAACGGT 900

Qy        929 CAGGATCAACAGTTGTACATTGGGATGGAAGTCCGGTCAGATTTAGATGCGGGT 988
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGGATCAACAGTTGTACATTGGGATGGAAGTCCGGTCAGATTTAGATGCGGGT 960

Qy        989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTCAAGAAGTCAAGAAACGTCGTA 1048
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGGGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTCAAGAAGTCAAGAAACGACGTCGTA 1020

Qy       1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1108
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1080

Qy       1109 ATCTTTCACGCCTCGTAACACTCTTCTTCTTTTTTTTTTTTTTTTGTTTGTTTAATAATT 1168
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db       1081 ATCTTTCACGCCTCGTAACACTCTTCTTC-TTTTTTTTTTTTTGTTTGTTTAATATT 1139

Qy       1169 TTTAAAACTTCCATTTCGTTTTCTTTATTTGCATCGGTTTCTTCTTTCTTCTTTCTTGTTTACCAA 1228
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1140 TTTAAAACTTCCATTTCGTTTTCTTTATTTGCATCGGTTTCTTCTTTCTTCTTTCTTGTTTACCAA 1199
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Qy    1229  AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT  1288
                 ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    1200  AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT  1259

Qy    1289  TTAAAAA  1295
                 ||||||
Db    1260  TTAAAAA  1266

RESULT 5
ABK65156
ID     ABK65156 standard; cDNA; 1281 BP.
XX
AC     ABK65156;
XX
DT     02-JUL-2002  (first entry)
XX
DE     Arabidopsis cDNA encoding a transcription factor #8.
XX
KW     Plant; ss; gene; transcription factor; transgenic; agriculture;
KW     metabolic chemical; environmental stress; drought;
KW     microbial disease resistance; herbicide resistance; seed yield;
KW     fruit yield; growth rate; leaf senescence; flower senescence.
XX
OS     Arabidopsis thaliana.
XX
PN     WO200215675-A1.
XX
PD     28-FEB-2002.
XX
PF     22-AUG-2001; 2001WO-US026189.
XX
PR     22-AUG-2000; 2000US-0227439P.
PR     16-NOV-2000; 2000US-00713994.
PR     18-APR-2001; 2001US-0083 7944.
XX
PA     (MEND-) MENDEL BIOTECHNOLOGY INC.
PA     (PILG/) PILGRIM M.
PA     (CREE/) CREELMAN R.
PA     (DUBE/) DUBELL A J.
PA     (HEAR/) HEARD J.
PA     (JIAN/) JIANG C.
PA     (KEDD/) KEDDIE J.
PA     (ADAM/) ADAM L.
PA     (RATC/) RATCLIFF O.
PA     (REUB/) REUBER J L.
PA     (RIEC/) RIECHMANN J L.
PA     (YUGG/) YU G.
PA     (PINE/) PINEDA O.
XX
PI     Pilgrim M, Creelman R, Dubell AJ, Heard J, Jiang C,   Keddie J;
PI     Adam L, Ratcliff O, Reuber JL, Riechmann JL,   Yu G,   Pineda O;
XX
DR     WPI; 2002-292022/33.
DR     P-PSDB; AAU92970.
XX
PT     An isolated or recombinant polynucleotide used to produce a transgenic
PT     plant.
XX
PS     Claim 4; Page 98-100; 941pp; English.
XX
CC     The invention relates to 1 of 232 isolated or recombinant polynucleotides
CC     encoding an Arabidopsis thaliana transcription factor, their variants,
CC     complements, fragments, or related polynucleotide with 31% to 95%
CC     sequence identity, where the plant possesses an altered trait as compared
CC     to a wild-type or reference plant, or the plant exhibits an altered
CC     phenotype as compared to a wild-type or reference plant, or the plant
CC     exhibits ectopic expression or altered expression of one or more genes
CC     associated with a plant trait as compared to a wild plant. Also included
CC     are a transgenic plant comprising the polynucleotide, a computer
CC     readable medium having stored sequence information, and identifying a
CC     homologue sequence from a database comprising a plurality of known plant
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CC     sequences comprising inputting sequence information selected from one of
CC     464 fully defined sequences given in the specification. The isolated or
CC     recombinant polynucleotide is used for producing a plant having a
CC     modified trait, the method comprising selecting a polynucleotide that
CC     encodes a polypeptide or an antisense nucleic acid, inserting the
CC     polynucleotide or antisense nucleic acid into an expression vector,
CC     introducing the vector into a plant or a cell of a plant to overexpress
CC     the polypeptide or antisense nucleic acid, thereby producing a modified
CC     plant, and selecting for a modified trait (e.g. increased production of
CC     agriculturally useful proteins or metabolic chemicals, pest tolerance,
CC     environmental stress response (e.g. drought), microbial disease
CC     resistance, herbicide resistance, seed and fruit yield, growth rate, leaf
CC     and flower senescence and many other traits listed in the specification).
CC     The present sequence is one of the 232 polynucleotides encoding an A.
CC     thaliana transcription factor
XX
SQ     Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match             95.9%;  Score 1255;  DB 6;  Length 1281;
Best Local Similarity   99.9%;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy     29  CACAACACAAACACATTTCTGTTTCTCCATTGTTCAAACCATAAAAAAAACACAGAT   88
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CACAACACAAACACATTTCTGTTTCTCCATTGTTCAAACCATAAAAAAAACACAGAT   60

Qy     89  TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACAGGTTCCATCTGTGAAACC  148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACAGGTTCCATCTGTGAAACC  120

Qy    149  CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA  208
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA  180

Qy    209  TCAAGCGTTGTGTTAGATTCAGAGAACCGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  268
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TCAAGCGTTGTGTTAGATTCAGAGAACCGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  240

Qy    269  TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAGACGGGAGCTCAGATTTACGAG  328
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAGACGGGAGCTCAGATTTACGAG  300

Qy    329  AAACACCAGCGCGTGCTGCTCGGGACATTCAACGAAGACAGAAGCCGCTCGTGCCTAC  388
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AAACACCAGCGCGTGCTGCTCGGGACATTCAACGAAGACAGAAGCCGCTCGTGCCTAC  360

Qy    389  GACGTCGGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  448
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GACGTCGGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  420

Qy    449  ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCGAATCGTTGATATG  508
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCGAATCGTTGATATG  480

Qy    509  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCGTAAACGCGGTCGTGTAATGGTAC  568
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCGTAAACGCGGTCGTGTAATGGTAC  540

Qy    569  GGAAACATGACTAGGACGTTGTTAACGTCGGGTTGAGTAATGATGATGTTTCTACGACG  628
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGAAACATGACTAGGACGTTGTTAACGTCGGGTTGAGTAATGATGATGTTTCTACGACG  600

Qy    629  GGGTTAGATCGGCGAGGCACTGTTGAGAAAGCGGTAACGCGGTTGGGAAG  688
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GGGTTAGATCGGCGAGGCACTGTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG  660

Qy    689  CTAAACCGTTGTTATACCGAAACATCACGAGAAACATTTCCGTACCGTCAGT  748
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTAAACCGTTGTTATACCGAAACATCACGAGAAACATTTCCGTACCGTCAGT  720

Qy    749  AACGTTCCGTGAAAGGAGTGTTGTTGAACTTTGGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AACGTTCCGTGAAAGGAGTGTTGTTGAACTTTGGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  780
```

PA   (ADAM/) ADAM L.
PA   (SAMA/) SAMAHA R.
XX
PI   Jiang C, Broun P, Riechmann JL, Pineda O, Zhang J, Yu G;
PI   Pilgrim M, Keddie J, Heard J, Reuber L, Ratcliffe O, Adam L;
PI   Samaha R;
XX
DR   WPI; 2003-555503/52.
DR   P-PSDB; ADA15449.
XX
PT   New transgenic plant comprising a recombinant polynucleotide, useful for
PT   altering a plant's trait for increasing plant stability.
XX
PS   Claim 14; SEQ ID NO 3; 159pp; English.
XX
CC   The invention discloses a transgenic plant having an A. thaliana
CC   recombinant polynucleotide (a transcription factor) comprising a sequence
CC   encoding a polypeptide with at least 6 consecutive amino acids of one of
CC   the amino acid sequences given in the specification. The recombinant
CC   polynucleotide alters a trait of the transgenic plant's roots when
CC   compared to the same trait of the roots of another plant lacking the
CC   recombinant polynucleotide. Also claimed are methods for altering the
CC   expression levels of at least one gene of a plant, altering a trait
CC   associated with a plant's roots and altering a plant's trait. The
CC   recombinant polynucleotide further comprises a promoter operably linked
CC   to the nucleotide sequence. The promoter is constitutive or inducible or
CC   root-active. The method for altering a trait associated with roots
CC   comprises transforming a plant with the recombinant polynucleotide,
CC   selecting the transformed plants and identifying a transformed plant with
CC   roots having an altered trait. The method for altering the expression
CC   levels of at least one gene of a plant comprises transforming a plant
CC   with the recombinant polynucleotide and selecting the transformed plant.
CC   The method for altering a trait associated with a plant's roots comprises
CC   transforming a plant with the recombinant polynucleotide and selecting
CC   the transformed plant. The method for altering a plant's trait comprises
CC   providing a database sequence comparing the database sequence with the
CC   polypeptide, selecting the database that meets selected sequence criteria
CC   and transforming the selected database sequence in the plant. The methods
CC   also comprise providing a test polynucleotide, hybridising the test
CC   polynucleotide with the recombinant polynucleotide at low stringency and
CC   transforming the hybridising test polynucleotide in a plant to alter a
CC   trait of the plant. The transgenic plant is useful for altering a plant's
CC   trait for increasing plant stability. The sequence presented is a DNA
CC   encoding a protein of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 9; Length 1281;
Best Local Similarity   99.9%; Pred. No. 4e-288;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy   29 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAACACAGAT 88
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCGTGAAACC 148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCGTGAAACC 120

Qy   149 CCGGGCGATAACTCCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGGCGATAACTCCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGTTGTTGTTAGATTCAGAGAACGCGCTAGAAGCGTGAATCTAGGAAGCTTCCGTCG 268
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTTGTTAGATTCAGAGAACGCGCTAGAAGCGTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAATACAAAGGGTGGTGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 328
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAATACAAAGGGTGGTGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGCAGAAGACGAAGAAGAGCGCGCTGTGCCTAC 388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGAATCTACCGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGAATCTACCGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGCGGT 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGCGGT 960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy 1049 GGAAACAAAAGAGTGAACGATACGAGATGTATCGTGGTGTGTAGCAAGAGCAACGC 1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GGAAACAAAAGAGTGAACGATGAACGATACTGAGATGTATCGTGGTGTGTAGCAAGAGCAACGC 1080

Qy 1109 ATCTTTCACGCCCTCGTAACAACTCTTCTTCTTTTTTTTTTTCTTTTGTTGTTTTTAATAATT 1168
          ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 1081 ATCTTTCACGCCCTCGTAACAACTCTTCTTC-TTTTTTTTTCTTTTGTTGTTTTTAATAATT 1139

Qy 1169 TTTAAAAACTCCATTTCGTTTCTTTATTGCATCGGTTTCTTCTTTCTTGTTTACCAA 1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1140 TTTAAAAACTCCATTTCGTTTCTTTATTGCATCGGTTTCTTCTTTCTTGTTTACCAA 1199

Qy 1229 AGGTTCATGAGTTGTTTTGTGTTGTTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1200 AGGTTCATGAGTTGTTTTGTGTTGTTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy 1289 TTAAAAA 1295
          |||||||
Db 1260 TTAAAAA 1266

RESULT 6
ADA15448
ID   ADA15448 standard; DNA; 1281 BP.
XX
AC   ADA15448;
XX
DT   06-NOV-2003 (first entry)
XX
DE   DNA encoding A. thaliana protein, SEQ ID NO:3.
XX
KW   Transgenic plant; plant; transcription factor; trait; root;
KW   plant stability; ds; gene.
XX
OS   Arabidopsis thaliana.
XX
PN   US2003061637-A1.
XX
PD   27-MAR-2003.
XX
PF   21-OCT-2002; 2002US-00278173.
XX
PR   23-MAR-1999; 99US-0125814P.
PR   22-MAR-2000; 2000US-00533393.
XX
PA   (JIAN/) JIANG C.
PA   (BROU/) BROUN P.
PA   (RIEC/) RIECHMANN J L.
PA   (PINE/) PINEDA O.
PA   (ZHAN/) ZHANG J.
PA   (YUGG/) YU G.
PA   (PILG/) PILGRIM M.
PA   (KEDD/) KEDDIE J.
PA   (HEAR/) HEARD J.
PA   (REUB/) REUBER L.
PA   (RATC/) RATCLIFFE O.

DT 23-SEP-2003 (first entry)
XX
DE A. thaliana cDNA encoding a disease tolerance transcription factor, G867.
XX
KW Plant; ss; gene; transcription factor; disease resistance; transgenic;
KW plant breeding; pathogens resistance; pests; resistance.
XX
OS Arabidopsis thaliana.
XX
PN US2003046723-A1.
XX
PD 06-MAR-2003.
XX
PF 22-MAR-2000; 2000US-0053029.
XX
PR 22-MAR-2000; 2000US-0053029.
XX
PA (HEAR/) HEARD J.
PA (BROU/) BROUN P.
PA (RIEC/) RIECHMANN J L.
PA (KEDD/) KEDDIE J.
PA (PINE/) PINEDA O.
PA (ADAM/) ADAM L.
PA (SAMA/) SAMAHA R.
PA (ZHAN/) ZHANG J.
PA (YUGG/) YU G.
PA (RATC/) RATCLIFFE O.
PA (PILG/) PILGRIM M.
PA (JIAN/) JIANG C.
PA (REUB/) REUBER L.
XX
PI Heard J, Broun P, Riechmann JL, Keddie J, Pineda O, Adam L;
PI Samaha R, Zhang J, Yu G, Ratcliffe O, Pilgrim M, Jiang C, Reuber L;
XX
DR WPI; 2003-521768/49.
DR P-PSDB; AB043125.
XX
PT New transgenic plants comprising a recombinant gene that alters the
PT plant's disease tolerance or resistance, useful in plant breeding, e.g.
PT for generating plants with improved tolerance or resistance to diseases,
PT pests or pathogens.
XX
PS Claim 14; Page 64; 124pp; English.
XX
CC The invention relates to a transgenic plant, comprising a recombinant
CC polynucleotide that alters the plant's disease tolerance or resistance
CC when compared with the same trait of another plant lacking the
CC recombinant polynucleotide. The recombinant polynucleotide comprises a
CC nucleotide sequence, which encodes a polypeptide comprising at least 6
CC consecutive amino acids of any of 56 transcription factor proteins
CC appearing as ABO43093-ABO43148. Also included are altering the disease
CC tolerance or resistance of a plant (by: (a) transforming a plant with the
CC recombinant polynucleotide; (b) selecting the transformed plants; and (c)
CC identifying a transformed plant with an altered disease tolerance or
CC resistance), altering the expression levels of at least one gene in a
CC plant by transforming the plant with the recombinant polynucleotide,
CC altering a plant's trait (comprising: (a) providing a database sequence;
CC (b) comparing the database sequence with the polypeptide or
CC polynucleotide cited above; (c) selecting a database sequence that meets
CC the selected sequence criteria; and (d) transforming the selected
CC database sequence in the plant) and altering a plant's trait (comprising:
CC (a) providing a test polynucleotide; (b) hybridising the test
CC polynucleotide at low stringency with the recombinant polynucleotide
CC cited above; and (c) transforming the hybridising test polynucleotide in
CC a plant to alter a trait of the plant. The transgenic plant is useful in
CC plant breeding, particularly for generating plants with improved
CC tolerance or resistance to diseases. The plants have commercial utility
CC for increasing tolerance or resistance to pathogens and pests. The
CC present sequence is an Arabidopsis thaliana transcription factor cDNA of
CC the invention
XX
SQ Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

```
Db   301  AAACACCAGCGCGTGTGGCTCGGGACACATTCAACGAAGAGACGAAGCCGCTCGTGCCTAC  360

Qy   389  GACGTCGCGGTTCACAGGTTCCGTCGGACGCCGTCACAAATTTCAAAGACGTGAAG       448
          |||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db   361  GACGTCGCGGTTCACAGGTTCCGTCGGCCGTGACGGCCGTCACAAATTTCAAAGACGTGAAG  420

Qy   449  ATGGACGAGACGAGGTCGATTTCTTGAATTCTCATTCGAGAATCTGAGATCGTTGATATG  508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ATGGACGAGACGAGGTCGATTTCTTGAATTCTCATTCGAGAATCTGAGATCGTTGATATG  480

Qy   509  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAATGGTAAC  568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAATGGTAAC  540

Qy   569  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  628
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  600

Qy   629  GGGTTTAGTACGGCGGAGGCACTGTTTGAGAAACGGTAACGCCAAGCGACGTGGGAAG  688
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAACGGTAACGCCAAGCGACGTGGGAAG  660

Qy   689  CTAAACCGTTGGTTATACCGGAGTGTTGTTGTTGAACATTTTCCGTTACCGTCAAGT  748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CTAAACCGTTGGTTATACCGGAGTGTTGTTGTTGAACATTTTCCGTTACCGTCAAGT  720

Qy   749  AACGTTTCCGTGAAAGAGGTGTTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AACGTTTCCGTGAAAGAGGTGTTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG  780

Qy   809  TTCCGTTACTCGTATTGGAACACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TTCCGTTACTCGTATTGGAACACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  840

Qy   869  TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTTAGTTTCAGTAGATCTAACGGT  928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTTAGTTTCAGTAGATCTAACGGT  900

Qy   929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT  988
          ||||||||||||||||||||||||||||||      ||||||||||||||||||||||||
Db   901  CAGGATCAACAGTTGTACATTGGGTGGAAGTCCGGGTCAGATTTAGATGCGGGT  960

Qy   989  CGGGTTTTGAGATTGTTCGGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA  1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  CGGGTTTTGAGATTGTTCGGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA  1020

Qy  1049  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTCGGTGGTCGTAGCAAGAAGCAACGC  1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTCGGTGGTCGTAGCAAGAAGCAACGC  1080

Qy  1109  ATCTTTCACGCCCGTAACAACTCCTTCTTCTTTTTTTTTCTTTTGTTCTTTTAATAATT  1168
          |||||||||||||||||||||   |||||||||||||||||||||||||| |||||||
Db  1081  ATCTTTCACGCCCGTAACAACTCCTTC-TTTTTTTTTCTTTTGTTCTTTTTAATAATT  1139

Qy  1169  TTTAAAAACTCCATTTCGTTTCTTTATTTCGTTTCTTTATTTCGTTTCTTTGTTTACCAA  1228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140  TTTAAAAACTCCATTTCGTTTCTTTATTTCGTTTCTTTATTTCGTTTCTTTGTTTACCAA  1199

Qy  1229  AGGTTCATGAGTTGTTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT  1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200  AGGTTCATGAGTTGTTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT  1259

Qy  1289  TTAAAAA  1295
          |||||||
Db  1260  TTAAAAA  1266
```

RESULT 7
ACD98391
ID   ACD98391 standard; cDNA; 1281 BP.
XX
AC   ACD98391;
XX
XX

```
Query Match      95.9%;   Score 1255;   DB 9;   Length 1281;
Best Local Similarity 99.9%;   Pred. No. 4e-288;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   1;

Qy      29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 88
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 60

Qy      89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC 120

Qy     149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCGGA 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCGGA 180

Qy     209 TCAAGCGTTGTGTTAGATTCAGAGAACCGGCTGAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCAAGCGTTGTGTTAGATTCAGAGAACCGGCTGAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy     269 TCAAAAATACAAAGTGTCGTGCCACAACCAAAACGGAAGATGGGAGCTTCAGATTTACGAG 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TCAAAAATACAAAGTGTCGTGCCACAACCAAAACGGAAGATGGGAGCTTCAGATTTACGAG 300

Qy     329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAAGCCCGTCGTGTGCCTAC 388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAAGCCCGTCGTGTGCCTAC 360

Qy     389 GACGTCGCCGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GACGTCGCCGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy     449 ATGGACGAAGACGAGGTCGATTTCATTCTTGAATTCTGAAATCTGAGATCGTTGATATG 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ATGGACGAAGACGAGGTCGATTTCATTCTTGAATTCTGAAATCTGAGATCGTTGATATG 480

Qy     509 TTGAGGAAACATACTTATACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TTGAGGAAACATACTTATACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy     569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy     629 GGGTTTAGATCGGCCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGTTGGGAAG 688
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGGTTTAGATCGGCCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGTTGGGAAG 660

Qy     689 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy     749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTGAGGACGTTAACGGAAAGTGTGGAGG 808
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTGAGGACGTTAACGGAAAGTGTGGAGG 780

Qy     809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTGTGTATGTTTCGGAACTAAAGGTTGACTCAGAGG 868
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTGTGTATGTTTCGGAACTAAAGGTTGACTCAGAGG 840

Qy     869 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTTGGATCTAACGGT 928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TTCGTTAAGGAGGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTTGGATCTAACGGT 900

Qy     929 CAGGATCAACAGTTGTACATTGGGTCGGAAGTCGAGATCCCGGGTCAGATTTAGATGCGGGT 988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CAGGATCAACAGTTGTACATTGGGTCGGAAGTCGAGATCCCGGGTCAGATTTAGATGCGGGT 960

Qy     989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy.:  1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1080

Qy    1109 ATCTTTCACGCCTCGTAACAACTCTCTTCTTCTTCTTCTTTTTCTTTTTGTTTTAATAATT 1168
           |||||||||||||||||||||||||||||||       |||||||||||||||||||||
Db    1081 ATCTTTCACGCCTCGTAACAACTCTCTTCTTC-TTTTTCTTTTTGTTTTAATAATT 1139

Qy    1169 TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCTTCTTCCTTCTTGTTTACCAA 1228
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1140 TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCTTCTTCCTTCTTGTTTACCAA 1199

Qy    1229 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTATTTATGGATAAATT 1288
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1200 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTATTTATGGATAAATT 1259

Qy    1289 TTAAAAA 1295
           |||||||
Db    1260 TTAAAAA 1266
```

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RESULT 8
ADB31784
ID   ADB31784  standard; DNA; 1281 BP.
XX
AC   ADB31784;
XX
DT   04-DEC-2003  (first entry)
XX
DE   DNA encoding plant (A. thaliana) transcription factor polypeptide #9.
XX
KW   Plant; transcription factor; transgenic plant; transgenic; plant trait;
KW   modified trait; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   US2003101481-A1.
XX
PD   29-MAY-2003.
XX
PF   15-NOV-2002; 2002US-00295403.
XX
PR   22-SEP-1998;  98US-0101349P.
PR   06-OCT-1998;  98US-0103312P.
PR   17-NOV-1998;  98US-0108734P.
PR   22-DEC-1998;  98US-0113409P.
PR   13-SEP-1999;  99US-00394519.
XX
PA   (ZHAN/)   ZHANG J.
PA   (FROM/)   FROMM M.
PA   (HEAR/)   HEARD J.
PA   (RIEC/)   RIECHMANN J L.
PA   (ADAM/)   ADAM L.
PA   (BROU/)   BROUN P.
PA   (PINE/)   PINEDA O.
PA   (REUB/)   REUBER L.
PA   (KEDD/)   KEDDIE J.
PA   (YUGG/)   YU G.
PA   (JIAN/)   JIANG C.
XX
PI   Zhang J, Fromm M, Heard J, Riechmann JL, Adam L, Broun P;
PI   Pineda O, Reuber L, Keddie J, Yu G, Jiang C;
XX
DR   WPI; 2003-597572/56.
DR   P-PSDB; ADB31785.
XX
PT   New isolated polypeptides and polynucleotide sequences, useful for
PT   screening a molecule to identify a molecule that modifies plant trait,
PT   and for producing plants with modified traits.
XX
PS   Claim 1; SEQ ID NO 17; 17pp; English.
XX
CC   The present invention relates to the isolation of plant (Arabidopsis
CC   thaliana) transcription factor polypeptide and polynucleotide sequences.
```

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CC   Also disclosed are: an expression vector comprising the isolated
CC   polynucleotide, a host cell comprising the expression vector, a
CC   transgenic plant comprising the isolated polynucleotide, a transgenic
CC   plant ectopically expressing the isolated polynucleotide or polypeptide,
CC   a method for screening a molecule to identify a molecule that modifies a
CC   plant trait by placing the molecule in contact with the plant, and
CC   monitoring the effect of the molecule on the expressing or activity of
CC   the polypeptide or polynucleotide, and producing a transgenic plant
CC   having a modified trait by ectopically expressing the isolated
CC   polypeptide and selecting a plant with the modified trait. The
CC   polypeptides, polynucleotides and methods are useful for screening a
CC   molecule to identify a molecule that modifies plant trait, and for
CC   producing plants with modified traits. The present sequence represents a
CC   plant transcription factor polynucleotide of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from the
XX   USPTO web site at seqdata.uspto.gov.
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match             95.9%;  Score 1255;  DB 10;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative   0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy     29 CACAACAACAAACACATTCTCCGTTTCTCCCATTGTTCCAAACCATAAAAAAAACACAGAT 88
          ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      1 CACAACAACAAACACATTCTCCGTTTCTCCCATTGTTCAAACCATAAAAAAAACACAGAT 60

Qy     89 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAGTTCCATCTGTGAAACC 148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAGTTCCATCTGTGAAACC 120

Qy    149 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy    209 TCAAGGCGTTGTGTTAGATTCAGAGAACGCCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCAAGGCGTTGTGTTAGATTCAGAGAACGCCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy    269 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 300

Qy    329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAAGCCGCTCGTGCCTAC 388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAAGCCGCTCGTGCCTAC 360

Qy    389 GACGTCGGCGGTTCACAGGTTCCGTCGCCGCGGTTCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGTCGGCGGTTCACAGGTTCCGTCGCCGCGGTTCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy    449 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTTCATTCGAAATCTGAGATCGTTGATATG 508
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTTCATTCGAAATCTGAGATCGTTGATATG 480

Qy    509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGCGTAAACGGCGTCGTAATGGTAAC 568
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGCGTAAACGGCGTCGTAATGGTAAC 540

Qy    569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTGATGATGGTGTTCTACGACG 628
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTGATGATGGTGTTCTACGACG 600

Qy    629 GGGTTTAGATCGGCGGAGGCACTGTTGAGAAAGCGGTTAACGCCAAGCGACGTTGGGAAG 688
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGGTTTAGATCGGCGGAGGCACTGTTGAGAAAGCGGTTAACGCCAAGCGACGTTGGGAAG 660

Qy    689 CTAAACCGGTTTGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTAAACCGGTTTGGTTATACCGAAACATCACGCAGAAACATCACGCAGAAACATTTTCCGTTACCGTCAAGT 720

Qy    749 AACGTTTCCGTGAAAGGAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTTTCCGTGAAAGGAGGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy    809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGAGCAGCAGG 868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGAGCAGCAGG 840

Qy    869 TTCGTTAAGGAGGAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGT 928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCGTTAAGGAGGAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy    929 CAGGATCAACAGTTGTACATTGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy    989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTCTTTTGTTGTTTAATAATT 1168
          |||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTCTTTTGTTGTTTAATAATT 1139

Qy   1169 TTTAAAAACTCCATTTCGTTTTCGTTTCTTTATTTGATCGGTTCTTCTTCTTGTTTACCAA 1228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TTTAAAAACTCCATTTCGTTTTCGTTTCTTTATTTGATCGGTTCTTCTTCTTGTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTTGTTGTTGTTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTTGTTGTTGTTATTGATGAACTGTAAATTTTATTTATAGGATAAAATT 1259

Qy   1289 TTAAAAA 1295
          |||||||
Db   1260 TTAAAAA 1266


RESULT 9
ADD55665
ID   ADD55665 standard; cDNA; 1281 BP.
XX
AC   ADD55665;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Thalecress environmental stress-related cDNA #12.
XX
KW   Thalecress; environmental stress; ss; gene; plant; viral infection;
KW   fungal infection; microbial infection; herbicide resistance; heat; cold;
KW   heavy metal; low light; drought; osmotic stress; salt concentration;
KW   transgenic.
XX
OS   Arabidopsis thaliana.
XX
PN   US2003131386-A1.
XX
PD   10-JUL-2003.
XX
PF   22-OCT-2002; 2002US-00278536.
XX
PR   23-MAR-1999;  99US-0125814P.
PR   22-MAR-2000; 2000US-00532591.
XX
PA   (SAMA/)   SAMAHA R.
PA   (HEAR/)   HEARD J.
PA   (JIAN/)   JIANG C.
PA   (PINE/)   PINEDA O.
PA   (REUB/)   REUBER L.
PA   (RIEC/)   RIECHMANN J L.
PA   (YUGG/)   YU G.
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```
PA   (KEDD/)  KEDDIE J.
PA   (RATC/)  RATCLIFFE O.
PA   (PILG/)  PILGRIM M.
PA   (ADAM/)  ADAM L.
PA   (BROU/)  BROUN P.
PA   (ZHAN/)  ZHANG J.
XX
PI   Samaha R, Heard J, Jiang C, Pineda O, Reuber L, Riechmann JL;
PI   Yu G, Keddie J, Ratcliffe O, Pilgrim M, Adam L, Broun P, Zhang J;
XX
DR   WPI; 2003-829608/77.
DR   P-PSDB; ADD55666.
XX
PT   New recombinant polynucleotide for altering the regulation of gene
PT   expression of plants to modify the plant's traits, particularly the
PT   plant's environmental stress tolerance.
XX
PS   Claim 14; SEQ ID NO 23; 219pp; English.
XX
CC   The invention relates to a recombinant polynucleotide that alters a
CC   plant's environmental stress tolerance when compared with the same trait
CC   of another plant lacking the recombinant polynucleotide. Also included
CC   are a transgenic plant comprising the novel recombinant polynucleotide
CC   having a sequence that encodes a polypeptide comprising at least 6
CC   consecutive amino acids of any of the 55 250-500 residue amino acid
CC   sequences (S1), given in the specification, altering the environmental
CC   stress response or tolerance of a plant, or altering a plant's trait and
CC   altering the expression levels of at least one gene in a plant. The
CC   recombinant polynucleotide and methods are useful for altering the
CC   regulation of gene expression of plants to modify the plant's traits, in
CC   particular with respect to environmental stress responses (e.g. to viral
CC   infection, fungal infection, microbial infection, herbicide resistance,
CC   heat, cold, heavy metals, low light, drought, osmotic stress and salt
CC   concentration). The present sequence is an environmental stress related
CC   polynucleotide of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match          95.9%;  Score 1255;  DB 10;  Length 1281;
Best Local Similarity  99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    29  CACAACACAAACACATTTCGTTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGAT  88
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CACAACAAACACACATTTCGTTTTCTCCATTGTTCAAACCATAAAAAAAAAACACAGAT  60

Qy    89  TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACAAGGTTCCATCTGTGAAACC  148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACAAGGTTCCATCTGTGAAACC  120

Qy   149  CCGGCGATAACTCCCGCGAAAAAGTCGTCGGTAGGTAGGTAACTTATACAGGATGGGAAGCGGA  208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CCGGCGATAACTCCCGCGAAAAAGTCGTCGGTAGGTAGGTAACTTATACAGGATGGGAAGCGGA  180

Qy   209  TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAGAAGCTTCCGTCG  268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAGAAGCTTCCGTCG  240

Qy   269  TCAAAATACAAAGGTGTGGTGCCACAACCAAACAAACGGAAGATGGGAAGCTCAGATTTACGAG  328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TCAAAATACAAAGGTGTGGTGCCACAACCAAACAAACGGAAGATGGGAAGCTCAGATTTACGAG  300

Qy   329  AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGACGAAGCCGCTCGTGCCTAC  388
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AAACACCAGCCGCGTGTGGCTCGGGACATTCAACGAAGACGAAGCCGCCGTGCCTAC  360

Qy   389  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  420

Qy   449  ATGGACGACGAAGACGAGGTCGATTCTCATTCGAAATCTGAAATCTGAGATCGTTGATATG  508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ATGGACGACGAAGACGAGGTCGATTCTCATTCGAAATCTGAAATCTGAGATCGTTGATATG  480

Qy   509  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACCGCTCGTAATGGTAAC  568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACCGCTCGTAATGGTAAC  540

Qy   569  GGAAACATGACTAGGACGTTGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGAAACATGACTAGGACGTTGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  600

Qy   629  GGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCGTAACGCCAAGCGTTGGAAG  688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCGTAACGCCAAGCGTTGGAAG  660

Qy   689  CTAAACCGTTGTTGGTTATACCGAAACATCACGCAGAGAAACATCTTTCCGTTACCGTCAAGT  748
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CTAAACCGTTGTTGGTTATACCGAAACATCACGCAGAGAAACATCTTTCCGTTACCGTCAAGT  720

Qy   749  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTGACGTTAACGGAAAGTGTGGAGG  808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTGACGTTAACGGAAAGTGTGGAGG  780

Qy   809  TTCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGAGCAGG  868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG  840

Qy   869  TTCGTTAAGGAGAAGAATCTACGTGCGTCGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT  928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TTCGTTAAGGAGAAGAATCTACGTGCGTCGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT  900

Qy   929  CAGGATCAACAGTTGTACATTGGGGTGGAAGTCGGAGTCAGATCCGGTCAGATTTAGATGCGGGT  988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  CAGGATCAACAGTTGTACATTGGGGTGGAAGTCGGAGTCAGATCCGGTCAGATTTAGATGCGGGT  960

Qy   989  CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGACGTCGTA  1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGACGTCGTA  1020

Qy  1049  GGAACAAAAAGAGTGAACGATACTGGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC  1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGAACAAAAAGAGTGAACGATACTGGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC  1080

Qy  1109  ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTTCTTTGTGTTTAATAATT  1168
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  1081  ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTCTTTGTGTTTAATAATT  1139

Qy  1169  TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTTCTTCTTTCTTTCTTGTTTACCAA  1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140  TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTTCTTCTTTCTTTCTTGTTTACCAA  1199

Qy  1229  AGGTTCATGAGTTGTTTTGTTGTGTATTGATGAGAACTGTAAATTTTATTTATTGGATAAAT  1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200  AGGTTCATGAGTTGTTTTGTTGTGTATTGATGAGAACTGTAAATTTTATTTATTGGATAAAT  1259

Qy  1289  TTAAAAA  1295
          |||||||
Db  1260  TTAAAAA  1266

RESULT 10
ADD30762
ID   ADD30762 standard; cDNA; 1281 BP.
XX
AC   ADD30762;
XX
DT   15-JAN-2004 (first entry)
XX
DE   Plant yield-related polynucleotide clone G867.
XX
KW   ds; transcription factor; transgenic plant; growth rate; senescence;
KW   seed germination rate; plant vigor; seedling vigor.
XX
OS   Arabidopsis thaliana.
XX
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PN   WO200303227-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-US025805.
XX
PR   09-AUG-2001; 2001US-0310847P.
PR   19-NOV-2001; 2001US-0336049P.
PR   11-DEC-2001; 2001US-0338692P.
PR   14-JUN-2002; 2002US-0171468.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI   Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;
PI   Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
PI   Broun PE;
XX
DR   WPI; 2003-248221/24.
DR   P-PSDB; ADD30763.
XX
PT   New plant transcription factor polynucleotides and polypeptides, useful
PT   in producing transgenic plants with commercially valuable properties,
PT   such as an alteration in a plant growth characteristic, e.g. growth rate
PT   or apomixis.
XX
PS   Disclosure; SEQ ID NO 791; 454pp; English.
XX
CC   The invention relates to a number of isolated Arabidopsis thaliana cDNA
CC   sequences and their encoded proteins which are especially transcription
CC   factor related cDNA's and proteins. The isolated or recombinant plant
CC   transcription factor polynucleotides and polypeptides are useful in
CC   producing transgenic plants with commercially valuable properties, i.e.
CC   modified or altered desirable traits as compared to a reference plant,
CC   such as an alteration in a plant growth characteristic, e.g. growth rate,
CC   germination rate of seeds, vigor of plants and seedlings, or leaf and
CC   flower senescence. Sequence information related to the polynucleotides
CC   and polypeptides can also be used in bioinformatic search methods. The
CC   transgenic plant is useful for growing a progeny plant from a parent
CC   plant. This sequence represents one of the cDNAs of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 10; Length 1281;
Best Local Similarity   99.9%; Pred. No. 4e-288;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

Qy   29 CACAACAACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 88
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CACAACAACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGTACTACACAAGTACTACACAGGTTCCATCGTGAAACC 148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGTACTACACAAGTACTACACAGGTTCCATCGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGTGTGCCACAACCAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGTGCCACAACCAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGAAGCGAAGCCGCTCGTGCCTAC 388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGAAGCGAAGCCGCTCGTGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTGCGCCCGTGCACAAATTTCAAAGACGTGAAG 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTGCGCCCGTGCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTCTCATTCGAAATTCGAGATCGTTGATATG 508
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGGTCGATTCTCATTCGAAATTCGAGATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTGAGTGAATGATGGTGTTCTTACGACG 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTGAGTGAATGATGGTGTTCTTACGACG 600

Qy   629 GGGTTTAGATCGGCGGAGGCACTGTTGAGAAAGCGTAACCGGCAAGCGACGTTGGGAAG 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTTAGATCGGCGGAGGCACTGTTGAGAAAGCGTAACCGGCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGGACGCGTTAACGGAAGTGTGGAG 808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGGACGCGTTAACGGAAGTGTGGAG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAGGTTGGAGCAGG 868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTCAGTTCAGATCTAACGGT 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTCAGTTCAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGAGCAAGAAGCAACGC 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCCTGTAACAACTCCTTCTTCTTTTGTTTGTTTTTAATAATT 1168
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   1081 ATCTTTCACGCCCTGTAACAACTCCTTCTTC-TTTTTTTTTCTTTTTGTTTGTTTTTAATAATT 1139

Qy   1169 TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGTTTCTTCTTGTTTACCAA 1228
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   1140 TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTTCTTGTTTTGTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTTGTTTTTGTGTATTGATGAACTGTAAATTTATTTATTAGGATAAATT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTTGTTTTTGTGTATTGATGAACTGTAAATTTATTTATTAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
          |||||||
Db   1260 TTAAAAA 1266

RESULT 11
ADE37198
ID   ADE37198 standard; cDNA; 1281 BP.
XX
AC   ADE37198;
XX
DT   29-JAN-2004 (first entry)
XX
DE   Plant yield related polynucleotide clone G867.
XX
KW   ds; gene; transcription factor; tolerance; environmental condition;

```
Qy   269  TCAAAATACAAAGGTGTGGTGCGCACCACCAAACGCGAGGATGGGAGCGAGCTCAGATTTACGAG  328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TCAAAATACAAAGGTGTGGTGCGCACCACCAAACGCGAGGATGGGAGCGAGCTCAGATTTACGAG  300

Qy   329  AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGAGCGAAGCCGTCGTCGTGCCTAC  388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGAGCGAAGCCGTCGTCGTGCCTAC  360

Qy   389  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG  448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG  420

Qy   449  ATGGACGAAGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ATGGACGAAGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  480

Qy   509  TTGAGGAAACATACTTATAACGAAGAGTTAGACGAGAGTAAACCGCGTCGTAATGGTAAC  568
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   481  TTGAGGAAACATACTTATAACGAAGAGTTAGACGAGAGTAAACCGGTCGTAATGGTAAC  540

Qy   569  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  600

Qy   629  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGGCCAAGCGACGTTGGGAGG  688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGGCCAAGCGACGTTGGGAGG  660

Qy   689  CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTTACCGTCAAGT  748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTTACCGTCAAGT  720

Qy   749  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGGAGGACGTTAACGGGAAAGTGTGGAGG  808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGGAGGACGTTAACGGGAAAGTGTGGAGG  780

Qy   809  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG  868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG  840

Qy   869  TTCGTTAACGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTTGGAGTCTAACGGT  928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TTCGTTAACGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTTGGAGTCTAACGGT  900

Qy   929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCAGATCCGGGTCAGATTTGAGATGCGGGT  988
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   901  CAGGATCAACAGTTGTACATTGGGTGGAAGTCAGATCCGGGTCAGATTTAGATGCGGGT  960

Qy   989  CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAACGACGACTCGTA  1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAACGACGACTCGTA  1020

Qy  1049  GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTGTGTGAGTCAAGAAGCAACGC  1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTGTGTGAGTCAAGAAGCAACGC  1080

Qy  1109  ATCTTTCACGCCTCGTAACAACTCTTCTTCTTC-TTTTTTTCTTTTGTTTGTTTAATAATT  1168
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1081  ATCTTTCACGCCTCGTAACAACTCTTCTTCTTCTTTTTTTCTTTTGTTTGTTTAATAATT  1139

Qy  1169  TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCTTTCTTTCTTTGTTTACCAA  1228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140  TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTCTTTCTTTCTTTGTTTACCAA  1199

Qy  1229  AGGTTCATGAGTTGTTTTTGTTATTGGTGATTGATGAACTGTAAATTTTATTTATTAGGATAAATT  1288
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200  AGGTTCATGAGTTGTTTTTGTTATTGGTGATTGATGAACTGTAAATTTTATTTATTAGGATAAATT  1259

Qy  1289  TTAAAAAA  1295
          ||||||||
Db  1260  TTAAAAAA  1266
```

KW   microbial disease; fungal disease; viral disease; pest infestation;
KW   herbicide sensitivity; heavy metal tolerance; heavy metal uptake;
KW   growth improvement; photocondition; nutrient uptake; hormone sensitivity;
KW   transgenic plant.
OS   Arabidopsis thaliana.
XX
FH   Key   Location/Qualifiers
FT   CDS   64..1098
FT   /tag= a
FT   /product= "transcription factor"
XX
PN   WO2003014327-A2.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-US026966.
XX
PR   09-AUG-2001; 2001US-0310847P.
PR   19-NOV-2001; 2001US-0336049P.
PR   11-DEC-2001; 2001US-0338692P.
PR   14-JUN-2002; 2002US-00171468.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI   Reuber TL, Riechmann JL, Heard JE, Jiang C, Adam LJ, Dubell AN;
PI   Ratcliffe O, Pineda O, Yu GL, Broun PB;
XX
DR   WPI; 2003-256576/25.
DR   P-PSDB; ADB37199.
XX
PT   New stress-related transcription factor polynucleotides and polypeptides,
PT   useful for producing transgenic plants with e.g. improved tolerance to
PT   diseases or pests, decreased herbicide sensitivity, or improved nutrient
PT   uptake.
XX
PS   Disclosure; SEQ ID NO 137; 470pp; English.
XX
CC   The invention relates to a number of cDNA sequence and their encoded
CC   proteins which are especially transcription factor cDNAs and their
CC   proteins. The isolated or recombinant polynucleotide is useful for
CC   producing a modified plant with a modified trait, e.g. enhanced tolerance
CC   to environmental conditions, improved tolerance to microbial, fungal or
CC   viral diseases, improved tolerance to pest infestation, decreased
CC   herbicide sensitivity, improved tolerance of heavy metals, or enhanced
CC   ability to take up heavy metals, improved growth under poor
CC   photoconditions, improved nutrient uptake, or reduced hormone
CC   sensitivity. The transgenic plants are useful for growing a progeny plant
CC   comprising the desired trait. The polynucleotides and polypeptides are
CC   also useful in bioinformatic search methods. This sequence represents one
CC   of the cDNAs of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 10; Length 1281;
Best Local Similarity   99.9%; Pred. No. 4e-288;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

```
Qy    29  CACAACACAAAACACATTCGTTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT   88
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CACAACACAAACACATTCGTTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT   60

Qy    89  TAAATGGAATCGAGTAGCGTTGATGAGTAGCTACTACCAAGTACAGAGTTCCATCTGAAACC   148
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TAAATGGAATCGAGTAGCGTTGATGAGTAGCTACTACCAAGTACAGAGTTCCATCTGTGAAACC   120

Qy   149  CCGGCGATAACTCCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA   208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CCGGCGATAACTCCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGA   180

Qy   209  TCAAGCGTTGTGTTGAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG   268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TCAAGCGTTGTGTTGAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG   240
```

```
Matches 1266; Conservative  0; Mismatches  0; Indels  1; Gaps  1;

Qy     29 CACAACAACAAACACATTCTGTTTCTCCATTGTTCAAACCATAAAAAAACACAGAT 88
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACAACAACAAACACATTCTGTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGAT 60

Qy     89 TAAATGAATCGAGTAGCGTTGATGAGAGTACTACAGTACTACAGTACTACAGTTCCATCTGTGAAACC 148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TAAATGAATCGAGTAGCGTTGATGAGAGTACTACAGTACTACAGTACTACAGTTCCATCTGTGAAACC 120

Qy    149 CCGGCGGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGGA 208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGGCGGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGGA 180

Qy    209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy    269 TCAAAATACAAAGGTGGTGCCACAACCAAACGGAGAATGGGAGCTCAGATTACGAG 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCAAAATACAAAGGTGGTGCCACAACCAAACGGAGAATGGGAGCTCAGATTACGAG 300

Qy    329 AAACACCAGCGCGTGTGGCTCCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAACACCAGCGCGTGTGGCTCCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy    389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTCACAAATTTCAAAGACGTGAAG 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCCGTCACAAATTTCAAAGACGTGAAG 420

Qy    449 ATGGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAAATCTCGAGATCGTTGATATG 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAAATCTCGAGATCGTTGATATG 480

Qy    509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy    569 GGAAACATGACTAGGACGTTGTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACG 628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGAAACATGACTAGGACGTTGTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACG 600

Qy    629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy    689 CTAAACCGTTGGTTATACCGGTGGAACATCAGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTAAACCGTTGGTTATACCGGTGGAACATCAGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy    749 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGGAAGTGTGGAGG 808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGGAAGTGTGGAGG 780

Qy    809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy    869 TTCGTTAAGGAGAAGATCTCACGTGCTGGTGACGTGGTTCAGTTCAGTTGAGATCTAACCGT 928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCGTTAAGGAGAAGATCTCACGTGCTGGTGACGTGGTAGTTCAGTTCAGTTGAGATCTAACCGT 900

Qy    929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy    989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1108
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1080
```

RESULT 12

AAD47502
ID   AAD47502 standard; DNA; 1281 BP.
XX
AC   AAD47502;
XX
DT   24-FEB-2003 (first entry)
XX
DE   Arabidopsis thaliana G867 transcription factor DNA.
XX
KW   Transcription factor; metabolite pathway; terpenoid; limonene synthase;
KW   alkaloid pathway gene; taxadiene synthase; biological pathway; freezing;
KW   abiotic stress; cold; drought; heat; nutrient deficiency; biotic stress;
KW   infection; developmental pathway; flowering; root development; TDS; LS;
KW   transgenic; transgenic plant; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
FH   Key   Location/Qualifiers
FT   CDS   64..1098
FT   /*tag= a
FT   /product= "Arabidopsis thaliana G867 transcription factor
FT   protein"
XX
PN   WO20274917-A2.
XX
PD   26-SEP-2002.
XX
PF   15-MAR-2002; 2002WO-US007999.
XX
PR   16-MAR-2001; 2001US-00810836.
XX
PA   (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI   Broun P;
XX
DR   WPI; 2003-018799/01.
DR   P-PSDB; AAE30051.
XX
PT   Determining whether one of several test transcription factor (TF)
PT   polynucleotides encodes pathway TF by determining expression from pathway
PT   gene promoter linked to reporter gene in a cell in presence of test
PT   polynucleotides.
XX
PS   Disclosure; Page 162-163; 221pp; English.
XX
CC   The present invention relates to a high-throughput method for identifying
CC   a polynucleotide which encodes a transcription factor for controlling the
CC   expression of one or more genes in a pathway. The method is useful for
CC   determining whether a member of a pool of test transcription factor
CC   polynucleotides encodes a biosynthetic pathway transcription factor or a
CC   primary metabolite pathway gene or a secondary metabolite pathway gene
CC   such as a terpenoid or alkaloid pathway gene transcription factor. It is
CC   also useful for determining whether a member of a pool of test encodes a
CC   Mentha sp. or Taxus sp. terpenoid pathway gene where the terpenoid
CC   pathway gene encodes limonene synthase (LS) or taxadiene synthase (TDS).
CC   It is also useful for identifying one or more transcription factors that
CC   activate one or more genes of a biological pathway of a plant, fungi or
CC   animal cell, where the biological pathway can be a biochemical pathway
CC   such as biosynthetic pathways for soluble and insoluble carbohydrates,
CC   for amino acids and a response pathway to abiotic stress such as cold,
CC   freezing, drought, heat, nutrient deficiency, pH or biotic stress such as
CC   fungal, viral or bacterial infection, developmental pathway such as
CC   flowering, root development, a response pathway to environmental cues
CC   such as light intensity and light quality, circadian rhythm. Sequences of
CC   the invention are used to generate transgenic plants. The present
CC   sequence is Arabidopsis thaliana G867 transcription factor DNA
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match   95.9%; Score 1255; DB 10; Length 1281;
Best Local Similarity   99.9%; Pred. No. 4e-288;

```
PT    methods.
XX
PS    Claim 1; SEQ ID NO 169; 435pp; English.
XX
CC    The invention describes a transgenic plant comprising a recombinant
CC    polynucleotide of any one of more than 500 nucleotide sequences fully
CC    defined in the specification or its complement. The method of the
CC    invention can be used to produced a plant having altered traits such as:
CC    enhanced tolerance to abiotic stress; glyphosphate tolerance; hormone
CC    sensitivity; disease resistance; sugar sensing; early or late flowering;
CC    altered flower structure, change in stem bifurcations, altered branching
CC    pattern, reduced apical dominance, reduced trichome density; lack of
CC    trichomes; reduced ectopic trichome development; altered trichome
CC    development; increase in trichome number; altered stem morphology;
CC    increased root growth; increased root hairs; altered seed development;
CC    altered cell proliferation or cell differentiation; rapid development;
CC    premature senescence; increased necrosis; increase in seedling or plant
CC    size; decreased plant size; leaf morphology; seed morphology; seed
CC    biochemistry; increase in root anthocyanins; increase in plant
CC    anthocyanins, or alteration in light response or shade avoidance. The
CC    transgenic plant, polynucleotides and polypeptides are useful in
CC    bioinformatic search methods. This sequence encodes a plant transcription
CC    factor that can be used in the creation of a transgenic plant with
CC    altered traits.
XX
SQ    Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match             95.9%;  Score 1255;  DB 12;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    29  CACAACACAAACACATTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAAACACAGAT   88
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  CACAACACAAACACATTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAAACACAGAT   60

Qy    89  TAAATGGAATGGAGTGGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  148
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  TAAATGGAATGGAGTGGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  120

Qy   149  CCGGCGGATAACTCCGGCGGAAAAAGTCGTCGGTAGGAACTATACAGGATGGGAAGCCGGA  208
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CCGGCGGATAACTCCGGCGGAAAAAGTCGTCGGTAGGAACTATACAGGATGGGAAGCCGGA  180

Qy   209  TCAAGCGTTGTGTTAGATTCAGAGAACCGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  268
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  TCAAGCGTTGTGTTAGATTCAGAGAACCGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  240

Qy   269  TCAAAATACAAAGGTGTGGCGTGGCCTCGGGACAATCAACCAAACCAAACGGAAGATGGGAG  328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TCAAAATACAAAGGTGTGGCGTGGCCTCGGGACAATCAACCAAACCAAACGGAAGATGGGAG  300

Qy   329  AAACACCAGCGCGGTGTGCGTGGGCTGGCGGAAGCAGAAGCGAGACCGCTCGTCGCCTAC  388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  AAACACCAGCGCGGTGTGCGTGGGCTGGCGGAAGCAGAAGCGAGACCGCTCGTCGCCTAC  360

Qy   389  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACCAAATTTCAAAGACGTGAAG  448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACCAAATTTCAAAGACGTGAAG  420

Qy   449  ATGGACGAAGACGAGAGTCGATTTCTTGAATTCTGAGATCTGAAATCTGAAATCTGATATG  508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ATGGACGAAGACGAGAGTCGATTTCTTGAATTCTGAGATCTGAAATCTGAAATCTGATATG  480

Qy   509  TTGAGGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC  568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TTGAGGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC  540

Qy   569  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG  600

Qy   629  GGGTTTAGATCGGCCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG  688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1109  ATCTTTCACGCCGCGTAACAACCTTCTTCTTTTTTTTTTCCTTTGTGTTTTAATAATT  1168
           ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db  1081  ATCTTTCACGCCGCGTAACAACCTTCTTC-TTTTTTTTTTTCTTTGTGTTTTAATAATT  1139

Qy  1169  TTTAAAAACTCCATTTCGTTTTCTTTATTTGCATCGGTTCTTCTTCTTGTTTACCAA  1228
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140  TTTAAAAACTCCATTTCGTTTTCTTTATTTGCATCGGTTCTTCTTCTTGTTTACCAA  1199

Qy  1229  AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT  1288
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200  AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT  1259

Qy  1289  TTAAAAA  1295
           |||||||
Db  1260  TTAAAAA  1266
```

```
RESULT 13
ADI41706
ID   ADI41706 standard; DNA; 1281 BP.
XX
AC   ADI41706;
XX
DT   22-APR-2004  (first entry)
XX
DE   Plant transcription factor polynucleotide #85.
XX
KW   transgenic; plant; enhanced tolerance to abiotic stress;
KW   glyphosphate tolerance; hormone sensitivity; disease resistance;
KW   sugar sensing; flowering; flower structure; stem bifurcation;
KW   branching pattern; apical dominance; trichome; cell proliferation;
KW   root growth; root hair; seed development; cell differentiation;
KW   cell differentiation; premature senescence; necrosis; plant size;
KW   leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW   plant anthocyanin; light response; shade avoidance; bioinformatic;
KW   transcription factor; gene; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   US2004019927-A1.
XX
PD   29-JAN-2004.
XX
PF   25-FEB-2003; 2003US-00374780.
XX
PR   18-APR-2001; 2001US-00837944.
XX
PA   (SHER/)  SHERMAN B K.
PA   (RIEC/)  RIECHMANN J L.
PA   (JIAN/)  JIANG C.
PA   (HEAR/)  HEARD J E.
PA   (HAAK/)  HAAKE V.
PA   (CREE/)  CREELMAN R A.
PA   (RATC/)  RATCLIFFE O.
PA   (ADAM/)  ADAM L J.
PA   (REUB/)  REUBER T L.
PA   (KEDD/)  KEDDIE J.
PA   (BROU/)  BROUN P E.
PA   (PILG/)  PILGRIM M L.
PA   (DUBB/)  DUBELL A N.
PA   (PINE/)  PINEDA O.
PA   (YUGG/)  YU G.
XX
PI   Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;
PI   Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;
PI   Pilgrim ML, Dubell AN, Pineda O, Yu G;
XX
DR   WPI; 2004-132245/13.
DR   P-PSDB; ADI41707.
XX
PT   New transgenic plant comprising a recombinant polynucleotide of any one
PT   of more than 500 nucleotide sequences, useful in bioinformatic search
```

```
Db    601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy    689 CTAAAACCGTTCGTTTGGTTATACCGAGAACATCACCGCAGAGAAACATTTCCGTTACCGTTCAAGT 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTAAAACCGTTCGTTTGGTTATACCGAGAACATCACCGCAGAGAAACATTTCCGTTACCGTTCAAGT 720

Qy    749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy    809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy    869 TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTGACGTGGTTAGTTCAGTAGATCTAACGGT 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTGACGTGGTTAGTTCAGTAGATCTAACGGT 900

Qy    929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGTCAGATTTAGATGCGGGT 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGTCAGATTTAGATGCGGGT 960

Qy    989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTGGTGTGTAGCAAGAAGCAACGC 1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTGGTGTGTAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTTGTGTTTAATAATT 1168
          ||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTTCTTTTGTTGTTTAATAATT 1139

Qy   1169 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGGTTTCTTCCTTCTTGTTTTACCAA 1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGGTTTCTTCCTTCTTGTTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTGTTGTATTGAACTGTAAATTTTATTTATAGGATAAATT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTGTTGTATTGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
          ||||||
Db   1260 TTAAAAA 1266
```

RESULT 14
ADO02166
ID   ADO02166 standard; cDNA; 1281 BP.
XX
AC   ADO02166;
XX
DT   01-JUL-2004 (first entry)
XX
DE   Thalecress transcription factor cDNA #290.
XX
KW   Thalecress; transcription factor; ss; gene; plant; transgenic;
KW   abiotic stress; cold tolerance; heat tolerance; drought; osmotic stress;
KW   phosphate limitation; potassium limitation; nitrogen limitation;
KW   hormone sensitivity; disease resistance; sugar sensing; seed germination;
KW   flowering; inflorescence architectural change;
KW   meristem cell differentiation; phyllotaxy; apical dominance;
KW   trichome development; seed development; premature senescence;
KW   delayed senescence; lethality; necrosis; plant size; leaf morphology;
KW   seed morphology; secondary metabolism; light response; shade avoidance.
XX
OS   Arabidopsis thaliana.
XX
PN   US2004045049-A1.
XX
PD   04-MAR-2004.
XX

PF   10-APR-2003; 2003US-00412699.
XX
PR   13-SEP-1999;   99US-00394519.
PR   21-JAN-2000; 2000US-00489976.
PR   17-FEB-2000; 2000US-00506720.
PR   22-MAR-2000; 2000US-00532591.
PR   22-MAR-2000; 2000US-00533029.
PR   22-MAR-2000; 2000US-00533030.
PR   22-MAR-2000; 2000US-00533392.
PR   22-MAR-2000; 2000US-00533648.
PR   06-APR-2000; 2000WO-US009448.
PR   16-NOV-2000; 2000US-00713994.
PR   27-MAR-2001; 2001US-00819142.
PR   17-APR-2001; 2001US-00837444.
PR   30-JAN-2002; 2002US-00958131.
PR   14-JUN-2002; 2002US-00171468.
PR   09-AUG-2002; 2002US-00225066.
PR   09-AUG-2002; 2002US-00225067.
PR   09-AUG-2002; 2002US-00225068.
PR   17-DEC-2002; 2002US-0434166P.
PR   25-FEB-2003; 2003US-00374780.
XX
PA   (ZHAN/) ZHANG J.
PA   (FROM/) FROMM M E.
PA   (HEAR/) HEARD J E.
PA   (RIEC/) RIECHMANN J L.
PA   (ADAM/) ADAM L J.
PA   (BROU/) BROUN P E.
PA   (PINE/) PINEDA O.
PA   (REUB/) REUBER T L.
PA   (KEDD/) KEDDIE J S.
PA   (YUGG/) YU G.
PA   (JIAN/) JIANG C.
PA   (SAMA/) SAMAHA R S.
PA   (PILG/) PILGRIM M L.
PA   (CREE/) CREELMAN R A.
PA   (DUBE/) DUBELL A N.
PA   (RATC/) RATCLIFFE O.
PA   (KUMI/) KUMIMOTO R.
PA   (SHER/) SHERMAN B K.
XX
PI   Zhang J, Fromm MB, Heard JE, Riechmann JL, Adam LJ, Broun PE;
PI   Pineda O, Reuber TL, Keddie JS, Yu G, Jiang C, Samaha RS;
PI   Pilgrim ML, Creelman RA, Dubell AN, Ratcliffe O, Kumimoto R;
PI   Sherman BK;
XX
DR   WPI; 2004-225755/21.
DR   P-PSDB; ADO02167.
XX
PT   New transgenic plant, useful in developing phenotypes with altered or
PT   improved characteristics or traits.
XX
PS   Claim 1; SEQ ID NO 579; 213pp; English.
XX
CC   The invention relates to a transgenic plant comprises a recombinant
CC   polynucleotide having a polynucleotide sequence or its complementary
CC   sequence comprising a sequence encoding a polypeptide, that initiates
CC   transcription (i.e. a transcription factor) from Arabidopsis, Soybean,
CC   Rice, Rape or Corn, comprising any of the sequences appearing as ADO01588
CC   -ADO03527 or ADO03530-ADO3559. Also included are using a transgenic
CC   plant to grow a progeny plant, an expression cassette (comprising a
CC   constitutive, inducible or tissue-specific promoter and a recombinant
CC   polynucleotide described above), a host cell comprising the expression
CC   cassette, producing a modified plant having a modified trait, identifying
CC   a factor that is modulated by or interacts with a polypeptide encoded by
CC   the polynucleotide sequence and identifying at least one downstream
CC   polynucleotide sequence that is subject to a regulatory effect of any of
CC   the polypeptides encoded by the polynucleotide described above. The
CC   transgenic plant is useful for producing a plant that has an altered
CC   trait e.g. an enhanced tolerance to abiotic stress (increased tolerance
CC   to chilling, germination in cold conditions,freezing tolerance, tolerance
CC   to heat, tolerance to drought, tolerance to osmotic stress, tolerance to
CC   salt, tolerance to phosphate limitation, tolerance to potassium

```
CC   limitation, decreased sensitivity to nitrogen limitation), altered
CC   hormone sensitivity, reduced sensitivity to abscisic acid, an altered
CC   response to ethylene, disease resistance, altered susceptibility to
CC   Botrytis, altered susceptibility to Fusarium, altered susceptibility to
CC   Erysiphe, altered susceptibility to Pseudomonas syringae, altered
CC   susceptibility to Sclerotinia, altered sugar sensing, improved seed
CC   germination and seedling vigor, early flowering, late flowering, extended
CC   period of flowering, an inflorescence architectural change, a change in
CC   stem bifurcations, a lack of a shoot meristem, reduced meristem cell
CC   differentiation, altered phyllotaxy, altered branching pattern, reduced
CC   apical dominance, reduced trichome density, ectopic trichome development,
CC   altered trichome development, altered stem morphology, increased root
CC   growth, increased root hairs, altered seed development, altered cell
CC   proliferation/cell differentiation, premature senescence, delayed
CC   senescence, lethality, increased necrosis, an increase in seedling or
CC   plant size, a change in leaf morphology, increased
CC   altered leaf development, increased leaf size and mass, glossy leaves,
CC   leaf cell expansion, change in seed morphology, altered seed coloration,
CC   increased seed size, decreased seed size, altered seed shape, change in
CC   leaf biochemistry, increased leaf wax, an alteration in leaf prenyl lipid
CC   content, increased leaf insoluble sugars, decreased leaf insoluble
CC   sugars, increased leaf anthocyanins, an alteration of leaf fatty acid
CC   content, an alteration of leaf glucosinolate content, change in seed
CC   biochemistry, an increase in seed oil content, decrease in seed oil
CC   content, increase in seed fatty acid content, decrease in seed fatty acid
CC   content, increase in seed protein content, decrease in seed protein
CC   content, alteration in seed prenyl lipid content, increase in seed
CC   sterols, upregulation of genes involved in secondary metabolism, increase
CC   in root anthocyanins, increase in plant anthocyanins, and alteration in
CC   light response or shade avoidance. The present sequence encodes a
CC   thalecress transcription factor of the invention.
XX
SQ   Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match             95.9%;  Score 1255;  DB 12;  Length 1281;
Best Local Similarity   99.9%;  Pred. No. 4e-288;
Matches 1266;  Conservative    0;  Mismatches   0;  Indels   1;  Gaps   1;

Qy     29 CACAACAAACACATTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAAACACAGAT 88
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CACAACAAACACATTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAAACACAGAT 60

Qy     89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTTCCATCTGTGAAACC 148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTTCCATCTGTGAAACC 120

Qy    149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy    209 TCAAGCGTTGTGTTAGATTCAGAGAACGGGCGTAGAAGCTGAATCTAGGAGGCTTCCGTCG 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCAAGCGTTGTGTTAGATTCAGAGAACGGGCGTAGAAGCTGAATCTAGGAGGCTTCCGTCG 240

Qy    269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
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Db    241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 300

Qy    329 AAACACCAGCCGCGTGGCCGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 388
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Db    301 AAACACCAGCCGCGTGGCCGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy    389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGAGCGCCGTCACAAATTCAAAGACGTGAAG 448
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGAGCGCCGTCACAAATTCAAAGACGTGAAG 420

Qy    449 ATGGGACGAAGACGAGCGAGTTCGATTTCTTGAATCTCATTCGAAATCTGAAATCGTTGATATG 508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGGACGAAGACGAGCGAGTTCGATTTCTTGAATCTCATTCGAAATCTGAAATCGTTGATATG 480

Qy    509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGTAGAGCAGTAAACGGCGTCGTAAATGGTAAC 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGTAGAGCAGTAAACGGCGTCGTAAATGGTAAC 540

Qy    569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG 600

Qy    629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy    689 CTAAACCGTTGGTTATACCGGAAACATCACGACAGAGAAACATTTTCCGTTACCGTCAAGT 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTAAACCGTTGGTTATACCGGAAACATCACGACAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy    749 AACGTTTCCGTGAAAGGAGTGTGTTGGAACTTTGAGGACGTTAACGGGAAAGTGTGGGAG 808
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTTTCCGTGAAAGGAGTGTGTTGGAACTTTGAGGACGTTAACGGGAAAGTGTGGGAG 780

Qy    809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy    869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy    929 CAGGATCAACAGTTGTACATTGGGCGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGCGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy    989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAGAGTTATCGTTCGTGTGAGCAAGAAGCAACGC 1108
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAGAGTTATCGTTCGTGTGAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTCTTTTGTGTTGTTTAATAATT 1168
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTC-TTTTTTTTCTTTTGTGTTGTTTAATAATT 1139

Qy   1169 TTTAAAACTCCATTTGTTTCTTATTTGCATCGGTTTCTTCTTCTGTTTTGTTTACCAA 1228
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TTTAAAACTCCATTTGTTTCTTATTTGCATCGGTTTCTTCTTCTGTTTTGTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
          |||||||
Db   1260 TTAAAAA 1266

RESULT 15
ADP67768
ID   ADP67768 standard; cDNA; 1281 BP.
XX
AC   ADP67768;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Arabidopsis thaliana G867 AP2 transcriptional factor cDNA.
XX
KW   Plant; transcriptional factor; TF; transgenic plant;
KW   abiotic stress tolerance; gene expression; gene regulator;
KW   diagnostic probe; transcription factor modulator;
KW   osmotic stress tolerance; mouse-ear cress; gene; ss.
XX
OS   Arabidopsis thaliana.
XX
FH   Key             Location/Qualifiers
FT   CDS             64..1098
```

FT　　/*tag= a
FT　　/product= "Arabidopsis thaliana transcriptional factor
　　　　protein"
XX
PN　US2004098764-A1.
XX
PD　20-MAY-2004.
XX
PF　14-OCT-2003; 2003US-00685922.
XX
PR　16-MAR-2001; 2001US-00810836.
XX
PA　(HEAR/)　HEARD J E.
PA　(RIEC/)　RIECHMANN J L.
PA　(CREE/)　CREELMAN R A.
PA　(RATC/)　RATCLIFFE O.
PA　(KUMI/)　KUMIMOTO R W.
PA　(GUTT/)　GUTTERSON N.
PA　(REUB/)　REUBER T L.
PA　(PINE/)　PINEDA O.
PA　(LIBB/)　LIBBY J M.
PA　(SHER/)　SHERMAN B K.
XX
PI　Heard JE, Riechmann JL, Creelman RA, Ratcliffe O, Kumimoto RW;
PI　Gutterson N, Reuber TL, Pineda O, Libby JM, Sherman BK;
XX
DR　WPI; 2004-439639/41.
DR　P-PSDB; ADP67769.
XX
PT　New recombinant or isolated polynucleotide, useful for producing a
PT　transgenic plant having increased tolerance to abiotic stress (e.g., heat
PT　tolerance, chilling tolerance, germination in heat, and germination in
PT　cold).
XX
PS　Claim 1; SEQ ID NO 1; 117pp; English.
XX
CC　The present invention relates to plant transcriptional factor (TF)
CC　polypeptides and their encoding polynucleotides. The invention is useful
CC　for producing a transgenic plant having increase tolerance to abiotic
CC　stress, for increasing a plant's tolerance to abiotic stress, for
CC　producing commercially valuable plants and crops, for recombinant
CC　production (i.e. expression) of proteins, as regulators of plant gene
CC　expression, as diagnostic probes and for identifying exogenous or
CC　endogenous modulators of the transcription factors. The invention is also
CC　useful for screening libraries of molecules or compounds for specific
CC　binding and for creating transgenic plants having increased osmotic
CC　stress tolerance. The present sequence is a plant transcriptional factor
CC　cDNA.
XX
SQ　Sequence 1281 BP; 379 A; 219 C; 326 G; 357 T; 0 U; 0 Other;

Query Match　　95.9%; Score 1255; DB 12; Length 1281;
Best Local Similarity　99.9%; Pred. No. 4e-288;
Matches 1266; Conservative　0; Mismatches　0; Indels　1; Gaps　1;

Qy　　29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 88
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 60

Qy　　89 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAGTTCCATCTGTGAAACC 148
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　61 TAAATGGAATCGAGTAGCCGTTGATGAGAGTACTACAAGTACACAGTTCCATCTGTGAAACC 120

Qy　　149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCCGGA 208
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCCGGA 180

Qy　　209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTGAGAAGCTTCCGTCG 268
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Db　　　181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTGAGAAGCTTCCGTCG 240

Qy　　269 TCAAAATACAAAGGTGTGTGCCACACAACCAAACGGAGAATGGGGAGCTCAGATTTACCAG 328
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　　241 TCAAAATACAAAGGTGTGTGCCACACAACCAAACGGAGAATGGGGAGCTCAGATTTACGAG 300

Qy　　329 AAACACCAGCGCGTGCGTCGGACATTCAACGAAGAAGAAGAAGCCGCTCGTCGTGCCTAC 388
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Db　　　301 AAACACCAGCGCGTGCGTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTCGTGCCTAC 360

Qy　　389 GACGTCGCGGTTCCGTCGCCGTGACGCCGTCACAACAAATTCAAAGACGTGAAG 448
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　361 GACGTCGCGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy　　449 ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAGATCGTTGATATG 508
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　421 ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy　　509 TTGAGGAAACATACTACTTGTATAACGAAGAGTTAGAGCAGTAAACGGCGTCGTAATGGTAAC 568
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Db　　　481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGTAAACGGCGTCGTAATGGTAAC 540

Qy　　569 GGAAACATGACTAGGACGTTGTTAACGTCGGGTTGAGTGTGTTAACGTGTTTCTACGACG 628
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　541 GGAAACATGACTAGGACGTTGTTAACGTCGGGTTGAGTGTGTTAACGTGTTTCTACGACG 600

Qy　　629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy　　689 CTAAACCGTTGGTTATACCGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　661 CTAAACCGTTGGTTATACCGGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy　　749 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　721 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy　　809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy　　869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGGACGTGGTTAGTTCAGTGAGATCTAACGGT 928
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGGACGTGGTTAGTTCAGTGAGATCTAACGGT 900

Qy　　929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGGT 988
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGGT 960

Qy　　989 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　　　961 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy　1049 GGAAACAAAAGAGTGAACGATACTGAGATGTATCGTTCGGTGTGTGTGTGTAGCAAGAAGCAACGC 1108
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1021 GGAAACAAAAGAGTGAACGATACTGAGATGTATCGTTCGGTGTGTGTGTGTAGCAAGAAGCAACGC 1080

Qy　1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTCTTCTTTTTTTTTTTGTTTGTTTTTAATAATT 1168
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Db　1081 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTC-TTTTTTTTTTTGTTTGTTTTTAATAATT 1139

Qy　1169 TTTAAAAACTTCCATTTTCGTTTCTTTATTTGCATCGTTTCTTCTTCTTGTTTTACCAA 1228
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Db　1140 TTTAAAAACTTCCATTTTCGTTTCTTTATTTGCATCGTTTCTTCTTCTTGTTTTACCAA 1199

Qy　1229 AGGTTCATGAGTTGTTTTTGTTTGTGTATTGGTAAATTTATTTATGAGAACTGTAAATTTATTTATAGGATAAATT 1288
　　　　　||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db　1200 AGGTTCATGAGTTGTTTTTGTTTGTGTATTGGTAAATTTATTTATGAGAACTGTAAATTTATTTATAGGATAAATT 1259

Qy　1289 TTAAAAA 1295
　　　　　|||||||
Db　1260 TTAAAAA 1266

Search completed: September 11, 2005, 00:07:03
Job time : 809.449 secs

us-10-632-436a-1.rng

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OM nucleic - nucleic search, using sw model

Run on: September 10, 2005, 23:24:56 ; Search time 254.949 Seconds
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Title: US-10-632-436A-1
Perfect score: 1308
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Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
              1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
              2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
              3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
              4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
              5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
              6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	1255	95.9	1281	4	US-09-533-029-65	Sequence 65, Appl
2	389.8	29.8	1239	4	US-09-810-836B-1	Sequence 1, Appli
3	170.2	13.0	563	4	US-09-640-211A-230	Sequence 230, App
4	142.2	10.9	365	4	US-09-640-211A-1189	Sequence 1189, Ap
5	118.6	9.1	378	4	US-09-640-211A-1421	Sequence 1421, Ap
6	112.2	8.6	521	4	US-09-640-211A-238	Sequence 238, App
7	112.2	8.6	521	4	US-09-640-211A-1210	Sequence 1210, Ap
8	58.2	4.4	612	4	US-09-902-540-1357	Sequence 1357, Ap
9	57.2	4.4	240	1	US-08-628-417-6	Sequence 6, Appli
10	55.8	4.3	751	4	US-09-533-029-81	Sequence 81, Appl
c | 11 | 55.4 | 4.2 | 7218 | 1 | US-08-232-463-14 | Sequence 14, Appl |
c | 12 | 55 | 4.2 | 362 | 4 | US-09-621-976-16010 | Sequence 16010, A |
c | 13 | 55 | 4.2 | 1696 | 1 | US-09-835-811-1 | Sequence 1, Appli |
c | 14 | 54.4 | 4.2 | 365 | 4 | US-09-621-976-16042 | Sequence 16042, A |
c | 15 | 54.4 | 4.1 | 371 | 4 | US-09-621-976-16048 | Sequence 16048, A |
c | 16 | 53.6 | 4.1 | 359 | 4 | US-09-621-976-16019 | Sequence 16019, A |
c | 17 | 53.6 | 4.1 | 2447 | 2 | US-09-014-969-14 | Sequence 14, Appl |
c | 18 | 53.6 | 4.1 | 3275 | 3 | US-09-370-838-151 | Sequence 151, App |
c | 19 | 53.6 | 4.1 | 3275 | 4 | US-09-854-133-151 | Sequence 151, App |
c | 20 | 53.4 | 4.1 | 396 | 4 | US-09-640-173-53 | Sequence 53, Appl |
c | 21 | 53.4 | 4.1 | 396 | 4 | US-09-713-550-53 | Sequence 53, Appl |
c | 22 | 53.4 | 4.1 | 396 | 4 | US-09-825-294-53 | Sequence 53, Appl |
c | 23 | 53.4 | 4.1 | 396 | 4 | US-09-970-966-53 | Sequence 53, Appl |
c | 24 | 53.2 | 4.1 | 359 | 4 | US-09-621-976-16008 | Sequence 16008, A |
c | 25 | 52.8 | 4.0 | 2262 | 4 | US-09-311-021-171 | Sequence 171, App |
c | 26 | 52.6 | 4.0 | 357 | 4 | US-09-621-976-16058 | Sequence 16058, A |
c | 27 | 52.2 | 4.0 | 441 | 4 | US-09-601-537-10 | Sequence 10, Appl |
c | 28 | 52.2 | 4.0 | 4121 | 4 | US-09-601-537-9 | Sequence 9, Appli |
c | 29 | 51.4 | 3.9 | 578 | 3 | US-09-602-877A-95 | Sequence 95, Appl |
c | 30 | 51.4 | 3.9 | 1117 | 3 | US-09-247-373B-33 | Sequence 33, Appl |
c | 31 | 51.4 | 3.9 | 1798 | 3 | US-09-797-906-1 | Sequence 1, Appli |
c | 32 | 51.2 | 3.9 | 1039 | 4 | US-09-902-540-1280 | Sequence 1280, Ap |
c | 33 | 51 | 3.9 | 144 | 1 | US-08-702-344-26 | Sequence 26, Appl |
c | 34 | 50.6 | 3.9 | 1459 | 4 | US-09-537-654-3 | Sequence 3, Appl |
c | 35 | 50.6 | 3.9 | 6671 | 1 | US-08-280-443-1 | Sequence 1, Appli |
c | 36 | 50.6 | 3.9 | 6671 | 1 | US-08-457-459-1 | Sequence 1, Appli |
c | 37 | 50.6 | 3.9 | 6671 | 1 | US-08-555-678-1 | Sequence 1, Appli |
c | 38 | 50.6 | 3.8 | 6671 | 5 | PCT-US95-02275-1 | Sequence 1, Appli |
c | 39 | 50 | 3.8 | 614 | 4 | US-09-902-540-1318 | Sequence 1318, Ap |
c | 40 | 49.8 | 3.8 | 2394 | 4 | US-09-800-729-33 | Sequence 33, Appl |
c | 41 | 49.4 | 3.8 | 2146 | 2 | US-10-003-392-3 | Sequence 3, Appli |
c | 42 | 49.4 | 3.8 | 6243 | 2 | US-09-056-075-1 | Sequence 1, Appli |
c | 43 | 49 | 3.7 | 1051 | 3 | US-09-245-041-10 | Sequence 10, Appl |
c | 44 | 49 | 3.7 | 1051 | 4 | US-09-358-055B-10 | Sequence 10, Appl |
c | 45 | 49 | 3.7 | 1051 | 4 | US-09-893-238-10 | Sequence 10, Appl |

ALIGNMENTS

RESULT 1
US-09-533-029-65

; Sequence 65, Application US/09533029
; Patent No. 664446
; GENERAL INFORMATION:
; APPLICANT: Heard, Jacqueline
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Keddie, James
; APPLICANT: Pineda, Omaira
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Reuber, Lynne
; TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-010
; CURRENT APPLICATION NUMBER: US/09/533,029
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 60/125,814
; EARLIER FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 65
;   TYPE: DNA
;   LENGTH: 1281
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: G867
US-09-533-029-65

Query Match   95.9%; Score 1255; DB 4; Length 1281;
Best Local Similarity   99.9%; Pred. No. 0;
Matches 1266; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy   29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 88
          |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACCGGTTCCATCTGTGAAACC 148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACCGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCCGA 208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

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Qy    209  TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTGAAGCTGAATCTAGGAAGCTTCCGTCG  268
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTGAAGCTGAATCTAGGAAGCTTCCGTCG  240

Qy    269  TCAAAATACAAAGGTGTGTGCCACCAACCAAACGGAGAGATGGGAGCTCAGATTTACCAG  328
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  TCAAAATACAAAGGTGTGTGCCACCAACCAAACGGAGAGATGGGAGCTCAGATTTACCAG  300

Qy    329  AAACACCAGCGCCGGTGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC  388
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  AAACACCACGCGCTGTGCGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC  360

Qy    389  GACGTCGGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  448
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GACGTCGGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG  420

Qy    449  ATGGACGAAGACGAGGTCCATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  508
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  480

Qy    509  TTGAGGAAACATACTTATAACGAAGAGTTAGACGCAGAGTAAACGGCGTCGTAATGGTAAC  568
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TTGAGGAAACATACTTATAACGAAGAGTTAGACGCAGAGTAAACGGCGTCGTAATGGTAAC  540

Qy    569  GGAAACAATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGAATGTGTTTCTACGACG  628
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  GGAAACAATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGAATGTGTTTCTACGACG  600

Qy    629  GGGTTTAGATCGGCGGAGCACTGTTGAGAAGCGGTAACGCCAAGCGGTTGGGAAG  688
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  GGGTTTAGATCGGCGGAGCACTGTTGAGAAGCGGTAACGCCAAGCGGTTGGGAAG  660

Qy    689  CTAAACCGTTTGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT  748
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGT  720

Qy    749  AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGACGTTAACGGGAAAGTGTGGAGG  808
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  AACGTTTCCGTGAAAGAGAGTGTTGAACTTTGAGACGTTAACGGGAAAGTGTGGAGG  780

Qy    809  TTCCGTTACTCGTATTGGAACAGTAGTCAGATGTTTTGACTAAAGGTTGGAGCAGG  868
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  TTCCGTTACTCGTATTGGAACAGTAGTCAGATGTTTTGACTAAAGGTTGGAGCAGG  840

Qy    869  TTGTTAAGGAGAAGAATCTACGTGCTGGAAGTCCGGGTCAGATTTCAGTTAGTAGATCTAACGGT  928
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTCGTTAAGGAGAAGAATCTACGTGCTGGAAGTCCGGGTCAGATTTCAGTTAGTAGATCTAACGGT  900

Qy    929  CAGGATCAACAGTTGTACATTGGGTGGAAGTCAGATTCCGGAGTTCAAGAAACGACGTCTA  988
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  CAGGATCAACAGTTGTACATTGGGTGGAAGTCAGATTCCGGAGTTCAAGAAACGACGTCTA  960

Qy    989  CGGGTTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCTA  1048
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  CGGGTTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCTA  1020

Qy   1049  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAGAAGCAACGC  1108
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAGAAGCAACGC  1080

Qy   1109  ATCTTCACGCCTCGTAACAACTCCTTCTTC--TTTTTTTTTTGTTTTTGTTTTTAATAATT  1168
                |||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db   1081  ATCTTCACGCCTCGTAACAACTCCTTCTTC-TTTTTTTTTTTTTGTTTTTGTTTTTTAATAATT  1139

Qy   1169  TTTAAAAACTCCATTTTCGTTTTCTTTATTGCATCGGTTTCGTTGTTACCAA  1228
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140  TTTAAAAACTCCATTTTCGTTTTCTTTTATTGCATCGGTTTCGTTGTTACCAA  1199

Qy   1229  AGGTTCATGAGTTGTTTTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT  1288
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200  AGGTTCATGAGTTGTTTTTGTGTTGATTGAACTGTAAATTTTATTTATAGGATAAATT  1259

Qy   1289  TTAAAAA  1295
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Db   1260  TTAAAAA  1266
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RESULT 2
US-09-810-836B-1
; Sequence 1, Application US/09810836B
; Patent No. 6835540
; GENERAL INFORMATION:
;   APPLICANT: Broun, Pierre
;   TITLE OF INVENTION: METHOD FOR MODIFYING A BIOSYNTHETIC
;   TITLE OF INVENTION: PATHWAY
;   FILE REFERENCE: 51442001200/MBI0032
;   CURRENT APPLICATION NUMBER: US/09/810,836B
;   CURRENT FILING DATE: 2001-03-16
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1239
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (6)...(1091)
;   OTHER INFORMATION: G993
US-09-810-836B-1

Query Match   29.8%; Score 389.8; DB 4; Length 1239;
Best Local Similarity   64.5%; Pred. No. 8.9e-100;
Matches 668; Conservative   0; Mismatches 322; Indels 45; Gaps 4;

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Qy    159  CTCCGGCGAAAAAGTCGTCGGTAGTAACTATACAGGATGGATGGGAAGCCGATCAAGCGTTG  218
                || |  |||| ||| | | |  |   || |  ||| || |  | ||  ||||| ||||
Db    103  CTTCTCCGCCGGCGACGTCGATGCGTCCTACAGAATGGGAAGACGGCGGCGGAAGCAGCGTCG  162

Qy    219  TGTTAGATTCAGAGAACGCGGCGTAGAAGCTTGAATCTAGGAAGCTTCCTCGTCGTCAAAATACA  278
                ||| ||| ||  || | || | || ||| | ||| || | | | ||||||| | ||
Db    163  TTTTGGATTCAGAGAACGCGTCGAGACCGAGTCACGTAAGCTTCCTCGTCGAAATATA  222

Qy    279  AAGGTGTGTGCCACCAACCAAACGGAGAGATGGGAGCTCAGATTTACGACTAAACACCAGC  338
                ||||||||||| |||| |||  |||||||||||||||||||||| ||||| ||||| |||
Db    223  AAGGCGTTGTGCCTCAGCCTAACGGAGATGGGAGCTCAGATTTACGACGAAGCATCAGC  282

Qy    339  GCGTGTGGCTCGGGACATTCAACGAAGAGACGAAGCCCGTCGTTACGACGTCGCGCG  398
                || | | ||||||||| || | |  |||||| | ||| | | |  || ||| |||
Db    283  GAGTTTGGCTCCGGGTACTTTCAACGAGGAGAGAAGAAGCGCGTCGTCTTACGCATCGCGCG  342

Qy    399  TTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAA---GACGTGAAGATGGACG  455
                ||||| |  | ||| ||| | ||| |||| | || |||||   | |||| ||| ||
Db    343  TGAGGAGATTCCGGCGCCGCGACCCGTCACTAACTTCAAATCTCAAATCTGAAGTTGATGGAAACG  402

Qy    456  AAGACGAGGTGAGTCGATTCTTCATTCGAAATTCTGAGATCGTTGTTGATATGTTGAGGA  515
                || | |||| | || | ||| || || | ||  | ||||  | |||| | |  |||||
Db    403  ACCCGAATCGGCGTTTTCTTTGACGCTCATTCTAAAGCTGATCGTGTGTGATATGTTGAGGA  462

Qy    516  AACATACTTATAACGAAGAGTTAGAGCGCAGTAAACGGCTCGTTAATGGTAACGGAAAACA  575
                || | | ||   | || | ||| | | || | || |  ||| | ||||| |||| | |
Db    463  AACACACTTACGCACCTTACGCCGATGAGTTTGAGCAGTAGAGAAGTTTGTTAACGGCGACGGAA  522

Qy    576  TGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGCGGGTTTA  635
                |||| | || || ||| || | | | |   | | ||  | | | | || ||  | |
Db    523  AACGCCTCGGGTTGGATGGGACGGGCGACGTGTTACGCGAAAGGTACCGGGTTTA------TTGA  570

Qy    636  GATCGGCGGAGGCACTGTTGAGAAAGCGGGTAACGCCAAGCGGTTGGGAAGCTAAACC  695
                || |  |  || |||| | || | | |||| | || ||| ||| | || || ||||| ||
Db    571  GAGCGCGTGAGGTTTGTTCGAAGACTGTTACGCCAGCGCTCGGGAAGCTGAACC  630

Qy    696  GTTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAACGTTT  755
                || |   || | || |||| || | |||| | | |  | | || || |||| || | |
Db    631  GTTTAGTGATACCGGAAACAACACGCGGAAGAAGAAGCATTTTCCGTTTCCGGTTACCGGAACC  690

Qy    756  CCGT--------------------------------------GAAAGGAGTAGTTGTTGAACTTTGAACTTGTTAACG  794
                ||||                                      |  || || | | ||| | | | || |
Db          CCGT--------------------------------------
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Db  700 GGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAG---TAACGTTTC  756
Qy  233 GGTGATCCCGAAGCAGCAGCGGAGAAGCACTTCCCGCTCCGCGGCGGCGGCGGCGGCGGAC  292
            ||| |||  ||| |   || | ||||| ||   |||| |||
Db  757 CGTGAAAGGAGTGTGTTGAACTTGAGGACGTTAACGGCCGGAGAAGTGTGGAGGTTCCGTTA  816
Qy  293 GATGAAGGGCGTACGTGCTCAACTTCGAGACGTCGGCGGGAAGGTGTGCGGTTCCGGTA  352
            |||||||  || |   || | |||| || ||||||
Db  817 CTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTTCGTTAA  876
Qy  353 TTCGTACTGGAACAAGCAGCCAGAGCTACGTGCTCACCAGGTTGGAGCCGGTTCGTGAA  412
            | |||  ||||||   |  ||||| ||        |||| ||| || |||||| ||
Db  877 GGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGATCA  936
Qy  413 GGAGAAGAGCCTGAAGGCCGGACGCACCGTCGTCGTCTGCTTCCAGCGGTCGACCCGGCCCGACAA  472
            |||||||   || |   || | ||  | |
Qy  937 ACAGTTGTACATTGGGTGGAAGTCGAG  963
Db  473 GCAGCTCTACATCGACTTCAAGCCGCG  499
             |||| | ||||  |   | || ||||
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RESULT 4
US-09-640-211A-1189
; Sequence 1189, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1189
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(365)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-211A-1189

Query Match   10.9%;   Score 142.2;   DB 4;   Length 365;
Best Local Similarity   69.1%;   Pred. No. 4.5e-30;
Matches   208;   Conservative   0;   Mismatches   90;   Indels   3;   Gaps   1;

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Qy  666 TAACGGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGAAACATCACGCAGAGA  725
Db    1 TGACGGTGATCCCGAAGCGACGTGGGGAAGCTCGAACCGCTGGTGATCCGTGAAAGTGTGTGAACTTTG  782
           || ||   | |  ||| ||||  || ||| |  ||||
Qy  726 AACATTTTCCGTTACCGTCAAG---TAACGTTTCCGTTACCGTCAAGCGACGTTGGGAAGCT  782
Db   61 AGCACTTCCCGCTCCGCGGCGGCGGCGGCGGCGGGTTCCGGTTACTACTGGAACAGTAGTAGTCAGAGTT  120
            | | || ||| |||||
Qy  783 AGGACGTTAACGGGGAAGTGTGGAGGTTCCGTTACTACTGGAACAGTAGTAGTCAGAGTT  842
Db  121 AGGACGTCGGCGGGAAGTGTGGCGGTGTGGGCGGGTTATTCGTACTGGAACAGCAGCCAGAGCT  180
            ||||||   ||||||||||||  ||
Qy  843 ATGTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGAGAGAATCAACAGTTGTACATTGGGTGGAAGTCGACG  902
Db  181 ACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGATCAACAAGCAGCAGTCAGCAGTCGA  240
Qy  903 TGGTTAGTTTGACTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGA  962
Db  241 CCGTNTGCTTCCAGCGGTCGTTCCAGAGAGGCCGACGGCGGGGAGGCTGGGAAGCTGAACCGGC  300
Qy  963 G  963
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Db  691 CGATGGGATGAATCCGTTCCGACGAAAGGCGTTTGATTAACTTGGAAGATAGAACAG  750
Qy  795 GGAAAGTGTGGAGGTTCCGTTACTCGTTACTCGTTATTGGAACAGTAGTCAGAGTTATGTTTGACTA  854
            ||||||||| ||||||||| ||| || || |   |||| ||| |  |||||| | |||||||| ||
Db  751 GGAAAGTGTGGCGGTTCCGTTACGTCGTTACTGCTCAACAGCAGTCAAAGTTACGTGTTGACCA  810
Qy  855 AAGGTTGGAGCAGGTTCGTTAAGAGAGAAGAATCTACGTGCTGTGTGGGTTAGTTTCA  914
            | || |||||| |||||||||| ||| ||||||||  |||| |  | || |||||||
Db  811 AGGGCTGGAGCCGGTTCGTTAAAGAGAAGAATCTTCGAGCCGGTGATGTGGTTTGTTTCG  870
Qy  915 GTAGATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAG  974
            | ||||||| | || ||| ||||| |||| |
Db  871 AGAGATCAACCGGACCAGCCGGCAATTGTATATCCACTGGAAAGTCCGGTCAGTCCGG  930
Qy  975 ATTTAGATGCGGGTCGGGTTTGGGATTGTTCCGGAGATTGTTCCGGAGTGTTAACATTTCACCGGAGTTCAA  1034
Db  931 TTCAGACTGTGGTTAGGCTATTCGGAGTCAACATTTCAATGTGAGTAACGAGAAACCAA  990
Qy  1035 GAAACAAAAGAGTGAAAGATGAACGATACTGAGATGTTATCGT  1085
                 ||||||   || |||||| |||||||| || ||||||| |||||
Db   991 ACGACGTCGCAGTTAGAGTGTGTTGGCAAGAAGAGATCTCCGGGAAGATGATTGTTTCGT  1050
Qy  1086 TGGTGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTT  1145
                 | ||||| ||||||||| || ||| |||||||      ||  | || |   |||||||
Db  1051 TAGGGTGTTCCAAGAAGCAGCGGCGATTATCAACATCTTGTGACAAATTCTTTTTTTTTTTTGT  1110
Qy  1146 TTTCTTTTGTTGTTT  1160
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Db  1111 TTTTTTTCTTCAATTT  1125
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RESULT 3
US-09-640-211A-230
; Sequence 230, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-230

Query Match   13.0%;   Score 170.2;   DB 4;   Length 563;
Best Local Similarity   61.5%;   Pred. No. 7.1e-38;
Matches   312;   Conservative   0;   Mismatches   183;   Indels   12;   Gaps   2;

```
Qy  460 CGAGGTCGATTCTTGAAATTCTCATTCGAAATCTGAAATCTGATATGTTGATGATCG  519
Db    2 CGAGGCCGACTTCCTGCCAAACACTTCCAGATCGTCGCAGATGCTCGCAGAAGCGCGCAAGCA  61
           ||||| ||| ||  ||   ||| ||||
Qy  520 TACTTATAACGAAGAGTAGAGCAGAGCAGAGCTAAGCGGCTAATGCGGCGTCGTAATGGTAACGGAAACATGAC  579
Db   62 CACGTACCGCGACGAGCTAGAGCAGCAAGCGGCTACAGGGGCTTCCGCCGCCGGAACG  121
Qy  580 TAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTTAGATC  639
Db  122 GGCCGGGAGGGGCCGGCCGGTTCGGCCGCGTAACGCCCGGACGGTGGTGGCGGCGGACA  240
Qy  640 GGCGGAGGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTT  699
Db  173 CCGTNTGCTTCCAGCGGTCGTTCCAGAGAGGCCGACGGCGGGGAGGCTGGGAAGCTGAACCGGCT  232
```

Db   301 G 301

RESULT 5
US-09-640-211A-1421
; Sequence 1421, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1421
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(378)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-211A-1421

Query Match   9.1%;   Score 118.6; DB 4;   Length 378;
Best Local Similarity   60.6%;   Pred. No. 2.2e-23;
Matches   234;   Conservative   0;   Mismatches 140;   Indels   12;   Gaps   2;

Qy   460 CGAGGTGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACA 519
                |||||| || | |||||||||||||||||| ||| |||||||||||||||
Db   2 CGAGGCGACTTCCTGGCCAAACACTCCAAGCCCGAGATCGTCGACATGCTCGCGCAAGCA 61

Qy   520 TACTTATAACGAAGAGTTAGAGCAGAGCTGGGGTAAACGCGTCGTAATGGTAACGAAGAGTTAGATC 579
                |||||| ||| |||||| ||||||||||||| |||| ||||||||||||||
Db   62 CACGTACCGCGACGAGCTAGAGCAGAGAGCAGAGCCAGCGTACACAGGGGTCGTTTCTACGACGGGGTTTAGATC 121

Qy   580 TAGGACGTTGTTAACGTCGGGGTGAGTAATGATGGTGTTTCTACGACGACGGGGTTTAGATC 639
                ||||||||||||||| ||||||| ||||||||||
Db   122 GGCCGGAGGGGCGGGGGTTCGGGGGGGGCGGACAGAGTGGTCGGCCCGGCG--------C 172

Qy   640 GGCGGAGGCACTGTTTGAGAAAGGGTAACGCCAAGCGACGTTGGGAGTCAAACCGTTT 699
                ||||||||||||||| |||||| |||||||||||||||||||
Db   173 CCGGGAGCAGCTGTTCGACGAGAAGGTACGCCGCCAGCGACGACGTGGGGAGTCAACCGGCT 232

Qy   700 GGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAG---TAACGTTTC 756
                || | | |||||||||||||||||||||||||| || ||||||
Db   233 GGTGATCCCGAAGCAGCANCACGCGGAGAAGCAGCCGTGCCCGCGCGGCGGGGGAAGTGTCGGCGGCGGGGGAAGTGTCGGCGGGAC 292

Qy   757 CGTGAAAGGAGTGTGTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTA 816
                ||||||| ||||||||||||||||||||||||||||||||||||
Db   293 GATGAAGGAGGGCGTACTGCTCAACTTCGAGAGACGTCGCGGCGGGAAGTGTGGCGGGTTCCCGGTA 352

Qy   817 CTCGTATTGGAACAGTAGTCAGAGTT 842
                ||||||||||||||||||
Db   353 TTCGTACTGGAACAGCAGCCAGAGCT 378

RESULT 6
US-09-640-211A-238
; Sequence 238, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription

; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-238

Query Match   8.6%;   Score 112.2; DB 4;   Length 521;
Best Local Similarity   66.8%;   Pred. No. 1.7e-21;
Matches   181;   Conservative   0;   Mismatches   78;   Indels   12;   Gaps   1;

Qy   644 GAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTT 703
                |||||||||||||||||| |||||||||||||||||||||||||||||
Db   246 GAGCCCATGTTCGAGAAGCCGCTGACGCCGAGCGACGTGGGGAAGCTGAACAGCGTGGTG 305

Qy   704 ATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTCCGTGAAA 763
                |||||||||| |||||||| |||| ||||||||||
Db   306 ATACCGAAGCAGCAGCGCCGGAGAAGCACTTCCCGCT---------GTGGGCGGAGGGCG 353

Qy   764 GGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTACTCGTAT 823
                |||||||| ||||||||||||||||||||||||| ||||||||||||||||||
Db   354 ACCCAGCAGCTGAGCTTCGAGGACGAGCGAGTGCGGGGAGTGTGGGAGTGTGGGAGGTTCCGCTACTCCTAC 413

Qy   824 TGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGCAGCTAAAGGTTCGAGGACAGAG 883
                || ||| |||| |||||| || || |||||||||||||
Db   414 TGGAGGCAGCAGCCAGACTACGTCCTCACCAAGGGCTGGAGCCGCTGGAGGTCGAGGACAGAG 473

Qy   884 AATCTACGTGCTCGTGACGTGGTTTAGTTTCA 914
                ||||
Db   474 CGCCTCGACGCGCCGGGGACGTGGTCCTCCTCA 504

RESULT 7
US-09-640-211A-1210
; Sequence 1210, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; TITLE OF INVENTION: Modification of Gene Transcription
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1210
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1210

Query Match   8.6%;   Score 112.2; DB 4;   Length 521;
Best Local Similarity   66.8%;   Pred. No. 1.7e-21;
Matches   181;   Conservative   0;   Mismatches   78;   Indels   12;   Gaps   1;

Qy   644 GAGGCACTGTTTGAGAAAGCGGTAACCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTT 703
                |||||||||||||||||| |||||||||||||||||||||||||||||
Db   246 GAGCCCATGTTCGAGAAGCCGCTGACGCCGAGCGACGTGGGGAAGCTGAACAGCGTGGTG 305

Qy   704 ATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAA 763
                |||||||||| |||||||| |||| ||||||||||
Db   306 ATACCGAAGCAGCAGCGCCGGAGAAGCACTTCCCGCT---------GTGGGCGGAGGGCG 353

Qy   764 GGAGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTACTCGTAT 823
                |||||||| ||||||||||||||||||||||||| ||||||||||||||||||
Db   354 ACCCAGCAGCTGAGCTTCGAGGACGAGCGAGTGCGGGGAGTGTGGGAGTGTGGGAGGTTCCGCTACTCCTAC 413

Qy   824 TGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGGTTCGTTAAGGAGAAG 883
                ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db   414 TGGAGCAGCAGCCAGAGCTACGTCCTCACCAAGGGCTGGAGCCGCTTCGTCGTCAAGGACAAG 473

Qy   884 AATCTACGTGCTGGTGACGTGGTAGTTTCA 914
                || || ||||||||||||||
Db   474 CGCCTCGACGCCGCGGGACGTGGTCCTCTTCA 504

RESULT 8
US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;   APPLICANT: Goldman, Barry S.
;   APPLICANT: Hinkle, Gregory J.
;   APPLICANT: Slater, Steven C.
;   APPLICANT: Wiegand, Roger C.
;   TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;   FILE REFERENCE: 38-10(158491)B
;   CURRENT APPLICATION NUMBER: US/09/902,540
;   CURRENT FILING DATE: 2001-07-10
;   PRIOR APPLICATION NUMBER: 60/217,883
;   PRIOR FILING DATE: 2000-07-10
;   NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Myxococcus xanthus
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(612)
;   OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match   4.4%;   Score 58.2; DB 4; Length 612;
Best Local Similarity   60.0%; Pred. No. 3.5e-06;
Matches 96; Conservative   0; Mismatches 64; Indels   0; Gaps   0;

Qy   1131 TCTTCTCCTCTTTTTTTTTTTTTTCTTTTGTTGTTTAATAATTTTAAAAACTCCATTTTCGTTT 1190
                |||||||||||||||||||| |||| || ||||||||||||| |||||
Db   330 TTTTTTTTTTTATTTAANTTTTTTTTTTTTTAATTTTTTTTTTATTTTTTTTA 271

Qy   1191 TCTTTATTTGCATCGGTTCTTCTTCCTTGTTACCAAAGGTTCATGAGTTGTTTTGTT 1250
                | |||||||||| ||||||| || || ||| ||||||||||| || ||||||
Db   270 TTTTTATTTTATTTTTTTTTTTATTTTTTTTTTTTTTTTTTTT 211

Qy   1251 GTATTGATGAACTGTAAATTTTATTATAGGATAAATTTT 1290
                | |||| |||| |||||||||||||| || || ||||
Db   210 TTTTTTTTATTTTTTTTTTTTTTTTTTTATTTT 171

RESULT 9
US-08-628-417-6/c
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
;   APPLICANT: GILLESPIE, DAVID
;   TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
;   TITLE OF INVENTION: POLYMERASE CHAIN REACTION
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
;   ADDRESSEE: DEFENSE COMMAND
;   STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
;   CITY: ABERDEEN PROVING GROUND
;   STATE: MARYLAND
;   COUNTRY: USA
;   ZIP: 21010-5423
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/628,417
;   FILING DATE:
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BIFFONI, ULYSSES J
;   REGISTRATION NUMBER: 39,908
;   REFERENCE/DOCKET NUMBER: DAM 398-94
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 410-671-1158
;   TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 240 bases
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: oligodeoxynucleotide
;   HYPOTHETICAL: NO
;   ANTI-SENSE: YES
US-08-628-417-6

Query Match   4.4%;   Score 57.2; DB 1; Length 240;
Best Local Similarity   58.0%; Pred. No. 3.8e-06;
Matches 101; Conservative   0; Mismatches 73; Indels   0; Gaps   0;

Qy   1131 TCTTCTCCTCTTTTTTTTTTTTTTCTTTTGTTGTTTAATAATTTTAAAAACTCCATTTTCGTTT 1190
                |||||||||||||||||||||||| |||| ||||||||||||||
Db   187 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 128

Qy   1191 TCTTTATTTGCATCGGTTCTTCTTCCTTGTTACCAAAGGTTCATGAGTTGTTTTGTT 1250
                | |||||||||| ||| || |||| ||||
Db   127 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 68

Qy   1251 GTATTGATGAACTGTAAATTTTATTATAGGATAAATTTTAAAAAGGGGTTACTT 1304
                || |||| |||| |||||||||||| || |||||||
Db   67 TTTTTTTTTTTTTTTTTTTTTTTTTAGTAAAATTATTTCTAAAGTTTTATT 14

RESULT 10
US-09-533-029-81
; Sequence 81, Application US/09533029
; Patent No. 6664446
; GENERAL INFORMATION:
;   APPLICANT: Heard, Jacqueline
;   APPLICANT: Broun, Pierre
;   APPLICANT: Riechmann, Jose-Luis
;   APPLICANT: Keddie, James
;   APPLICANT: Pineda, Omaira
;   APPLICANT: Adam, Luc
;   APPLICANT: Samaha, Raymond
;   APPLICANT: Zhang, James
;   APPLICANT: Yu, Guo-Liang
;   APPLICANT: Ratcliffe, Oliver
;   APPLICANT: Pilgrim, Marsha
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Reuber, Lynne
;   TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
;   FILE REFERENCE: MBI-010
;   CURRENT APPLICATION NUMBER: US/09/533,029
;   CURRENT FILING DATE: 2000-03-22
;   EARLIER APPLICATION NUMBER: 60/125,814
;   EARLIER FILING DATE: 1999-03-23
;   NUMBER OF SEQ ID NOS: 121
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 751
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   OTHER INFORMATION: G25

US-09-533-029-81
Query Match 4.3%; Score 55.8; DB 4; Length 751;
Best Local Similarity 59.6%;
Matches 115; Conservative 0; Mismatches 72; Indels 6; Gaps 1;

```
Qy  275 TACAAAGTGTGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGA------G 328
            |||||||      |||||     |||||      |    ||
Db  227 TACAGAGGGATAAGGCAGAGGCCATGGGCAGCCGGAGATTCGTGACCCGAGC 286

Qy  329 AAACACCAGCCGCGTGTCGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 388
            |||       ||||  |||||||      |||||||
Db  287 AAAGGTGTACGTGTCTGGCTTGGCACATTCAAAACCCGACGACGTGCTCGAGCCTAC 346

Qy  389 GACGTCGCGGTTCACAGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
            |||||||   |||||     |||   |||   ||||||
Db  347 GACGTTGCTGCCATCAAAATCCTGCCGGAAAGCCAAACTGAATTTCCAAACACTCAA 406

Qy  449 ATGGACGAAGACG 461
            |||||  ||||||
Db  407 GTAGAAGAAGAAG 419
```

RESULT 11
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F.G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
Query Match 4.2%; Score 55.4; DB 1; Length 7218;

Best Local Similarity 4.7%; Pred. No. 9.3e-05;
Matches 17; Conservative 203; Mismatches 139; Indels 0; Gaps 0;

```
Qy   66 AAACCATAAAAAAAACACAGATTAAATGAATGATGAGTAGCGTTGATGAGAGTACTACAA 125
           ::.  ::::::::::. .::  :: .:: . ::.  :: :::: .:: .:
Db 1399 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1340

Qy  126 GTACAGGTTCCATCTGTGAAACCCGCGATAACTCCGGCGAAAAAGTCGTCGTAGTA 185
           : ::: . :::::::::  :: .::: :::::::
Db 1339 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1280

Qy  186 ACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCCTAGAAG 245
           :  :::::::::::::::::::::::
Db 1279 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1220

Qy  246 CTGAATCTAGGAGCTTCCGTCGTGACGCCGTCACAAATACAAAGGTGTGCCACAAACCGGAA 305
           :::    :::: . . ::: :::::::::::
Db 1219 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1160

Qy  306 GATGGGGAGCTCAGATTTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAG 365
           :: :: .::  .::::: :: ::: :::::::::::::
Db 1159 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1100

Qy  366 AAGACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCCGTCGCCGTGACGCC 424
           :: ::::::: . :: ::: ::::::::::::::::::
Db 1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAGCC 1041
```

RESULT 12
US-09-621-976-16010/c
; Sequence 16010, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16010
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16010
Query Match 4.2%; Score 55; DB 4; Length 362;
Best Local Similarity 58.4%; Pred. No. 2.1e-05;
Matches 94; Conservative 1; Mismatches 66; Indels 0; Gaps 0;

```
Qy 1130 CTCTTCTTCTTTTTTTTCTTTTGTTGTTTAATAATTTTAAAAACTCCATTTTCGTT 1189
           |||||||||||||||||||||||||||      ||||  |||||
Db  362 YTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 303

Qy 1190 TTCTTTATTTGCATCGGTTCTTCTTCTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTGT 1249
           |||||||||       ||||||||||||||  |||||||
Db  302 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCATAGAATGAATGAGGCTTGGTTGTTTTTA 243

Qy 1250 TGTATTGATGAACTGTAAATTTTATTTATTATAGGATAAATTTT 1290
           ||||||||       ||||||||||| |||||
Db  242 AATTTTTTCTATTTCTATTATTTTTCTATCGAATTATTTTT 202
```

RESULT 13
US-09-835-811-1/c
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND

```
;   TITLE OF INVENTION: USES THEREOF
;   FILE REFERENCE: CL0012228
;   CURRENT APPLICATION NUMBER: US/09/835,811
;   CURRENT FILING DATE: 2001-04-17
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 1
;   LENGTH: 1696
;   TYPE: DNA
;   ORGANISM: Human
US-09-835-811-1

Query Match             4.2%;   Score 55; DB 4;  Length 1696;
Best Local Similarity  57.1%;   Pred. No. 5.1e-05;
Matches  100;  Conservative  0;  Mismatches  75;  Indels  0;  Gaps  0;

Qy    1131 TCTTCTCTTTTTTTTTTTTCTTTGTTGTTTAATAATTTTAAAAACTCCATTTCGTTT 1190
                ||||| ||||||||||| |||| ||  || |||||||||||||||||||| |||| |||
Db    1668 TTTTTTTTTTTTTTTTTTTTTTTTT                                 1609

Qy    1191 TCTTTATTTGCATCGGTTCTTCTCTGTTTACCAAAGGTTCATGAGTTGTTTTTGTT 1250
                || |||| ||   |||||||||||||||||||||||||||||||||| ||||||||
Db    1608 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT                           1549

Qy    1251 GTATTGATGAACTGTAAATTTATTATAGGATAAATTTTAAAAAGGGTTACTTA 1305
                | ||| |||| || ||||| |||  |||||||||||||||||||||||||||
Db    1548 TTTTTTTTTTTTTTTTTTTTTTTTTTTAATCTATACAGTGATCCTTA 1494


RESULT 14
US-09-621-976-16042/c
;  Sequence 16042, Application US/09621976
;  Patent No. 6639063
;  GENERAL INFORMATION:
;  APPLICANT:  Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
;  SEQ ID NO 16042
;   LENGTH: 365
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-16042

Query Match             4.2%;   Score 54.4; DB 4;  Length 365;
Best Local Similarity  58.8%;   Pred. No. 3e-05;
Matches   94;  Conservative  0;  Mismatches  66;  Indels  0;  Gaps  0;

Qy    1131 TCTTCTCTTTTTTTTTTTCTTTGTTGTTTAATAATTTTAAAAACTCCATTTCGTTT 1190
                |||||| |||||||||| |||| ||  || |||||||||||||||||||| ||||
Db     361 TTTTTTTTTTTTTTTTTTTTTTT                                   302

Qy    1191 TCTTTATTTGCATCGGTTCTTCTCTGTTTACCAAAGGTTCATGAGTTGTTTTTGTT 1250
                || |||| |||    |||||||||||||||||||||||||| |||||||||||||
Db     301 TTTTTTTTTTTTTTTTTTTTTTTCATAGAATGAGGCTTGGTTTGTTTTTTTAA 242

Qy    1251 GTATTGATGAACTGTAAATTTATTATTATAGGATAAATTTT 1290
                | ||| |||| ||   |||||||||||||||||||||||
Db     241 ATTTTTTCTATTTCTATTATTTTCTATCGAATTATTTTT 202


RESULT 15
US-09-621-976-16048/c
;  Sequence 16048, Application US/09621976
;  Patent No. 6639063
;  GENERAL INFORMATION:
;  APPLICANT:  Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
```

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;   APPLICANT:  Giordano, J.Y.
;   TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;   FILE REFERENCE: GENSET.054PR2
;   CURRENT APPLICATION NUMBER: US/09/621,976
;   CURRENT FILING DATE: 2000-07-21
;   NUMBER OF SEQ ID NOS: 19335
;   SOFTWARE: Patent.pm
;   SEQ ID NO 16048
;   LENGTH: 371
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-621-976-16048

Query Match             4.2%;   Score 54.4; DB 4;  Length 371;
Best Local Similarity  58.8%;   Pred. No. 3.1e-05;
Matches   94;  Conservative  0;  Mismatches  66;  Indels  0;  Gaps  0;

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Db     302 TTTTTTTTTTTTTTTTTTTTTTTCATAGAATGAGGCTTGGTTTGTTTTTTTAA 243

Qy    1251 GTATTGATGAACTGTAAATTTATTATTATAGGATAAATTTT 1290
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Db     242 ATTTTTCTATTTCTATTATTTTCTATCGAATTATTTTT 203


Search completed: September 11, 2005, 02:57:38
Job time : 259.949 secs
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          GenCore version 5.1.6
     Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:       September 11, 2005, 02:51:01 ; Search time 1002.55 Seconds
                                  (without alignments)
                            8568.071 Million cell updates/sec

Title:         US-10-632-436A-1
Perfect score: 1308
Sequence:      1 gtatacatatacacacaacata........ttaaaagggttacttagat 1308

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters:    14702500

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Published Applications NA:*
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       11:  /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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       23:  /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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       26:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1308	100.0	1308	18	US-10-632-436A-1	Sequence 1, Appli
2	1278	97.7	1325	18	US-10-425-114-14526	Sequence 14526, A
3	1255	95.9	1281	10	US-09-533-029-65	Sequence 65, Appl
4	1255	95.9	1281	10	US-09-934-455-15	Sequence 15, Appl
5	1255	95.9	1281	14	US-10-278-173-3	Sequence 3, Appli
6	1255	95.9	1281	15	US-10-295-403-17	Sequence 17, Appl
7	1255	95.9	1281	15	US-10-278-536-23	Sequence 23, Appl

8	1255	95.9	1281	17	US-10-225-068-137	Sequence 137, App
9	1255	95.9	1281	17	US-10-225-066A-795	Sequence 795, App
10	1255	95.9	1281	17	US-10-374-780A-169	Sequence 169, App
11	1255	95.9	1281	18	US-10-412-699B-579	Sequence 579, App
12	1255	95.9	1281	18	US-10-685-922-1	Sequence 1, Appli
13	1255	95.9	1281	21	US-10-225-068-137	Sequence 137, App
14	1255	95.9	1281	22	US-10-225-066A-795	Sequence 795, App
15	1035	79.1	1035	9	US-09-938-842A-2316	Sequence 2316, Ap
16	1035	79.1	1035	11	US-09-938-842A-2316	Sequence 2316, Ap
17	1035	79.1	1035	22	US-10-996-058-35	Sequence 35, Appl
18 c	971.8	74.3	1003	9	US-09-770-445-229	Sequence 229, App
19	517.8	39.6	1002	22	US-10-996-058-37	Sequence 37, Appl
20	517.8	39.6	1078	18	US-10-425-114-14556	Sequence 14556, A
21	517.8	39.6	1155	10	US-09-934-455-35	Sequence 35, Appl
22	517.8	39.6	1155	17	US-10-225-068-77	Sequence 77, Appl
23	517.8	39.6	1155	17	US-10-225-066A-419	Sequence 419, App
24	517.8	39.6	1155	17	US-10-225-067-31	Sequence 31, Appl
25	517.8	39.6	1155	17	US-10-374-780A-369	Sequence 369, App
26	517.8	39.6	1155	18	US-10-412-699B-1891	Sequence 1891, Ap
27	517.8	39.6	1155	18	US-10-685-922-7	Sequence 7, Appli
28	517.8	39.6	1155	21	US-10-225-068-77	Sequence 77, Appl
29 c	517.8	39.6	1155	22	US-10-225-066A-419	Sequence 419, App
30	493.8	37.8	969	18	US-10-685-922-41	Sequence 41, Appl
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32	389.8	29.8	1239	10	US-09-934-455-413	Sequence 413, App
33	389.8	29.8	1239	14	US-10-278-173-5	Sequence 5, Appli
34	389.8	29.8	1239	15	US-10-295-403-35	Sequence 35, Appl
35	389.8	29.8	1239	17	US-10-225-066A-577	Sequence 577, App
36	389.8	29.8	1239	17	US-10-374-780A-2071	Sequence 2071, Ap
37	389.8	29.8	1239	18	US-10-412-699B-1827	Sequence 1827, Ap
38	389.8	29.8	1239	18	US-10-685-922-5	Sequence 5, Appli
39	389.8	29.8	1239	22	US-10-225-066A-577	Sequence 577, App
40	378.4	28.9	1246	10	US-09-934-455-345	Sequence 345, App
41	378.4	28.9	1246	14	US-10-278-173-123	Sequence 123, App
42	378.4	28.9	1246	15	US-10-295-403-7	Sequence 7, Appli
43	378.4	28.9	1246	15	US-10-278-536-171	Sequence 171, App
44	378.4	28.9	1246	17	US-10-225-066A-587	Sequence 587, App
45	378.4	28.9	1246	17	US-10-374-780A-1949	Sequence 1949, Ap

ALIGNMENTS

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RESULT 1
US-10-632-436A-1
; Sequence 1, Application US/10632436A
; Publication No. US20040078852A1
; GENERAL INFORMATION:
;  APPLICANT: Michael F. Thomashow
;  APPLICANT: Sarah George Fowler
;  APPLICANT: Jonathan Vogel
;  APPLICANT: Daniel Zarka
;  TITLE OF INVENTION: Transcription Factors to Improve Plant Stress Tolerance
;  FILE REFERENCE: 21835-00004
;  CURRENT APPLICATION NUMBER: US/10/632,436A
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: 60/400,777
;  PRIOR FILING DATE: 2002-08-02
;  NUMBER OF SEQ ID NOS: 2
;  SEQ ID NO 1
;    LENGTH: 1308
;    TYPE: DNA
;    ORGANISM: Arabidopsis thaliana
;    FEATURE:
;    NAME/KEY:
;    LOCATION:
;    OTHER INFORMATION: This is a cDNA sequence derived from mRNA encoding the putative
;    OTHER INFORMATION: AP2 domain transcription factor RAV1 (locus tag: At1g13260).
;    OTHER INFORMATION: The RAV1 coding sequence consists of nucleotides 92 through 1126
;    OTHER INFORMATION: numbered below.
US-10-632-436A-1

  Query Match             100.0%;  Score 1308;  DB 18;  Length 1308;
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Best Local Similarity 100.0%; Pred. No. 6.3e-294; Indels 0; Gaps 0;
Matches 1308; Conservative 0; Mismatches 0;

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Qy    181 AGTAACTTATACAGGATGGGAAGCGGATCAAGCGTGTGTTAGATTCAGAGAACGGCGT     240
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Qy    421 CGCCGTCACAAATTTCAAAGACGTGAAGATGACGAGACGAGGTCGATTTCTTGAATTC     480
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Qy    481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGA     540
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Db    481 TCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGA     540

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Db    541 GCAGAGTAAACGACGTCGTAATGTAACGGAAACATGACTAGGACGTTGTTAACGTCGGG     600

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Qy    721 AGAGAAGACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGTGTTGTGAACTT     780
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RESULT 2
US-10-425-114-14526
; Sequence 14526, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14526
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB22-009-A10_FLI
US-10-425-114-14526

Query Match   97.7%; Score 1278; DB 18; Length 1325;
Best Local Similarity   100.0%; Pred. No. 6.1e-287;
Matches 1278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     91 AATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCGTGAAACCCC        150
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Qy    211 AAGCGTTGTTAGATTCAGAGAACGGCGCCAACCAAACGGAAGATGGGAGCTCAGATTACGAGAA     270
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Qy    271 AAAATACAAAGGTGTGCCACAAACGGAAGATGGGGAAGTC     330
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Qy    331 ACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGAGCCGCTGCCTACGA     390
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Db    301 ACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGAGCCGCTGCCTACGA     360

Qy    391 CGTCGCGGTTCCACAGGTTCCGTCCGGGATCGTGAACAATTTCAAAGACGTGAAGAT     450
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```

APPLICANT: Pineda, Omaira
APPLICANT: Adam, Luc
APPLICANT: Samaha, Raymond
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Reuber, Lynne

TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-010
CURRENT APPLICATION NUMBER: US/09/533,029
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 60/125,814
EARLIER FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 1281
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G867
US-09-533-029-65

Query Match 95.9%; Score 1255; DB 10; Length 1281;
Best Local Similarity 99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db    1 CACAACACAAACACATTTCTGTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGAT  60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
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Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120

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Qy  209 TCAAGCGTTGTTTAGATTCAGAGAACGGGCGTAGAGCGTGAATCTAGGAAGCTTCCGTCG 268
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Db  181 TCAAGCGTTGTTTAGATTCAGAGAACGGGCGTAGAGCGTGAATCTAGGAAGCTTCCGTCG 240

Qy  269 TCAAAATACAAAGGTGTGTGCCAAACCAAACGGAAGATGGGAGCTCAGATTTACGAG 328
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Qy  329 AAACACCAGCGCGTGGCTCGGACATTCAACGAAGCAGAAGCAGAGCGCCGCTCGTGCCTAC 388
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Db  301 AAACACCAGCGCGTGGCTCGGACATTCAACGAAGCAGAAGCAGAGCGCCGCTCGTGCCTAC 360

Qy  389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGCTCACAAATTTCAAAGACGTGAAG 448
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Db  361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGCTCACAAATTTCAAAGACGTGAAG 420

Qy  449 ATGGACGAAGCGAGGTCGATTTCGAATTCTCATTCGAAATCTGAGATCGTTGATATG 508
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Db  421 ATGGACGAAGCGAGGTCGATTTCGAATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy  509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy  569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG 628
         ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db  541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTAGACG 600

Qy  629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660
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(left column continuation)

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Db  361 CGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCGCTGACAAATTTCAAAGACGTGAAGAT 420
         |||||||||||||||||||||||||||||||
Qy  451 GGACGAAGCGAGGTCGATTTCGAATTCTCATTCGAAATCTGAGATCGTTGATATGTT 510
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GGACGAAGCGAGGTCGATTTCGAATTCTCATTCGAAATCTGAGATCGTTGATATGTT 480

Qy  511 GAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGG 570
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGG 540

Qy  571 AAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACGGG 630
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 AAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACGGG 600

Qy  631 GTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCT 690
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCT 660

Qy  691 AAACCGTTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAA 750
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AAACCGTTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAA 720

Qy  751 CGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAAGTGTGGAGGTT 810
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 CGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAAGTGTGGAGGTT 780

Qy  811 CCGGTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTT 870
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 CCGGTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGGTT 840

Qy  871 CGTTAAGGAGAAGAATCTACGTCGGTCGGTTAGTTTCAGTAGATCTAACGGTCA 930
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 CGTTAAGGAGAAGAATCTACGTCGGTCGGTTAGTTTCAGTAGATCTAACGGTCA 900

Qy  931 GGATCAACAGTTGTACATTGGGGTCGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCG 990
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GGATCAACAGTTGTACATTGGGGTCGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCG 960

Qy  991 GGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTAGG 1050
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 GGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTAGG 1020

Qy 1051 AAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGCAACGCAT 1110
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 AAACAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGCAACGCAT 1080

Qy 1111 CTTTCACGCGCTCGTAACAACTCTTCTTCTTCTTCTTTTGTTCTTTAATAATTTT 1170
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 CTTTCACGCGCTCGTAACAACTCTTCTTCTTCTTCTTTTGTTCTTTAATAATTTT 1140

Qy 1171 TAAAAACTCCATTTTCGTTTTCTTATTTGCATCGGTTTCTTCTTGTTTACCAAAG 1230
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141 TAAAAACTCCATTTTCGTTTTCTTATTTGCATCGGTTTCTTCTTGTTTACCAAAG 1200

Qy 1231 GTTCATGAGTTGTGTTTTGTTGTTATTGATGAACTGTAAATTTATTTATAGGATAAATTTT 1290
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 GTTCATGAGTTGTGTTTTGTTGTTATTGATGAACTGTAAATTTATTTATAGGATAAATTTT 1260

Qy 1291 AAAAAGGGGTTACTTAGAT 1308
         |||||||||||||||||||
Db 1261 AAAAAGGGGTTACTTAGAT 1278
```

RESULT 3
US-09-533-029-65
; Sequence 65, Application US/09533029
; Publication No. US20030046723A1
; GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Brown, Pierre
APPLICANT: Riechmann, Jose-Luis
APPLICANT: Keddie, James

```
;     SOFTWARE: PatentIn version 3.1
;
;     SEQ ID NO 15
;     LENGTH: 1281
;     TYPE: DNA
;     ORGANISM: Arabidopsis thaliana
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: (64)..(1098)
;     OTHER INFORMATION: G867
US-09-934-455-15

Query Match             95.9%;    Score 1255;  DB 10;    Length 1281;
Best Local Similarity   99.9%;    Pred. No. 1.3e-281;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy          29 CACAACAAACACATTCTGTTTCTCCATTGTTTCAAACCATAAAAAAACACAGAT     88
                |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db           1 CACAACAAACACATTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT   60

Qy          89 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAGTAGACGGTTCCATCGTGAAACC    148
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAGTAGACGGTTCCATCGTGAAACC    120

Qy         149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCCGA    208
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCCGA    180

Qy         209 TCAAGCGGTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG    268
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TCAAGCGGTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG    240

Qy         269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG    328
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG    300

Qy         329 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGCGAAGCCGCTCGTCGTGCCTAC    388
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AAACACCAGCGCGTGTGCTCGGGACATTCAACGAAGCGAAGCCGCTCGTCGTGCCTAC    360

Qy         389 GACGTTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG    448
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 GACGTTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG    420

Qy         449 ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATG    508
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATG    480

Qy         509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC    568
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC    540

Qy         569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGGTTCTACGACG    628
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGGTTCTACGACG    600

Qy         629 GGGTTTGAGTCGGCGAGGCACTGTTTGAGAAAGCGGTAACCGCCAAGCGACGTTGGGAAG    688
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGGTTTGAGTCGGCGAGGCACTGTTTGAGAAAGCGGTAACCGCCAAGCGACGTTGGGAAG    660

Qy         689 CTAAACCGTTGGTTATACCGTTCCGTTACCGTCAAGT    748
                |||||||||||||||||||||||||||||||||||||
Db         661 CTAAACCGTTGGTTATACCGTTCCGTTACCGTCAAGT    720

Qy         749 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGACGTTGGAGTGTGGAGG    808
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGACGTTGGAGTGTGGAGG    780

Qy         809 TTCCGTTACTCGTATTGGAACAGTAGTTCAGAGTTTGACTAAAGGTTCGAGCAGG    868
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 TTCCGTTACTCGTATTGGAACAGTAGTTCAGAGTTTGACTAAAGGTTCGAGCAGG    840

Qy         869 TTCGTTAAGGAGAAGAATCTACGTGCTCGGTGGTGACGTGGTTAGTTTCAGTTGAGATCTAACCGT    928
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TTCGTTAAGGAGAAGAATCTACGTGCTCGGTGGTGACGTGGTTAGTTTCAGTTGAGATCTAACCGGT    900

Qy         929 CAGGATCAACAGTTGTACATTGGGTGGTGAAGTCGAGATCGCCGGGTCAGATTTAGATGCGGGGT    988
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 CAGGATCAACAGTTGTACATTGGGTGGTGAAGTCGAGATCGCCGGGTCAGATTTAGATGCGGGGT    960

Qy         989 CGGGTTTTGAGATTGTTCGGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA    1048
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 CGGGTTTTGAGATTGTTCGGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA    1020

Qy        1049 GGAAACAAAAGAGTGAACGACTACTGAGATGTTATCGTTGGTGTGTAGGCAGAAGCAACGC    1108
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GGAAACAAAAGAGTGAACGACTACTGAGATGTTATCGTTGGTGTGTAGGCAGAAGCAACGC    1080

Qy        1109 ATCTTTCACGCGCCTCGTAACAACTCCTTCTC-TTTTTTCTTTGTTGTTTAATAATT    1168
                ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        1081 ATCTTTCACGCGCCTCGTAACAACTCCTTCTC-TTTTTTCTTTGTTGTTTTAATAATT    1139

Qy        1169 TTTAAAAACTCCATTTCGTTTCTTATTGCATCGGTTTCTTTCTTTCTTGTTTACCAA    1228
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1140 TTTAAAAACTCCATTTCGTTTCTTATTGCATCGGTTTCTTTCTTTCTTGTTTACCAA    1199

Qy        1229 AGGTTCATGATGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT    1288
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1200 AGGTTCATGATGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT    1259

Qy        1289 TTAAAAA 1295
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Db        1260 TTAAAAA 1266
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RESULT 4
US-09-934-455-15
; Sequence 15, Application US/09934455
; Publication No. US20030121070A1
; GENERAL INFORMATION:
;   APPLICANT: Adam, Luc
;   APPLICANT: Creelman, Robert
;   APPLICANT: Dubell, Arnold
;   APPLICANT: Heard, Jacqueline
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Keddie, James
;   APPLICANT: Pilgrim, Marsha
;   APPLICANT: Ratcliffe, Oliver
;   APPLICANT: Reuber, Lynne
;   APPLICANT: Riechmann, Jose Luis
;   APPLICANT: Yu, Guo-Liang
;   APPLICANT: Pineda, Omaira
;   TITLE OF INVENTION: Genes for Modifying Plant Traits IV
;   FILE REFERENCE: MBI-0025
;   CURRENT APPLICATION NUMBER: US/09/934,455
;   CURRENT FILING DATE: 2001-08-22
;   PRIOR APPLICATION NUMBER: 60/227439
;   PRIOR FILING DATE: 2000-08-22
;   PRIOR APPLICATION NUMBER: MBI-0022
;   PRIOR FILING DATE: 2001-11-16
;   PRIOR APPLICATION NUMBER: MBI-0023
;   PRIOR FILING DATE: 2001-04-17
;   NUMBER OF SEQ ID NOS: 516

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Db      1 CACAACACAAACACATTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 60

Qy     89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGTTCCATCTGTGAAACC 148
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGTTCCATCTGTGAAACC 120

Qy    149 CCGGCGATAACTCCGGCGAAAAGTCGTCGGTAGGTAACTTATCAGGATGGGAAGCGGA 208
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATCAGGATGGGAAGCGGA 180

Qy    209 TCAAGCGTGTGTTGAGATTCAGAGAAGCGCGTAGAAGCGTGAATCTAGGAAGCTTCCGTCG 268
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCAAGCGTGTGTTGAGATTCAGAGAAGCGCGTAGAAGCGTGAATCTAGGAAGCTTCCGTCG 240

Qy    269 TCAAAATACAAAGGTGTGTGCCACAACCGAAGAGTGGGAGCTCAGATTTACGAG 328
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCAAAATACAAAGGTGTGTGCCACAACCGAAGAGTGGGAGCTCAGATTTACGAG 300

Qy    329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGCGAAGCCCGTCGTCGTGCCTAC 388
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGAGCGAAGCCCGTCGTCGTGCCTAC 360

Qy    389 GACGTCGCGGTTCCACAGGTTCCGTCGCCCGTGAGCGCCGTCACAAATTTCAAAGACGTGAAG 448
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GACGTCGCGGTTCCACAGGTTCCGTCGCCCGTGAGCGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy    449 ATGGACGAAGACAGAGGTCGATTCGTCATTCGAAATCTGAAATCTGAGATCGTTGATATG 508
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ATGGACGAAGACAGAGGTCGATTCGTCATTCGAAATCTGAAATCTGAGATCGTTGATATG 480

Qy    509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy    569 GGGAAACATGACTAGGACGTTGTTAACGTCCGGGGTTGAGTAATGATGGTGTTCTACGACG 628
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGAAACATGACTAGGACGTTGTTAACGTCCGGGGTTGAGTAATGATGGTGTTCTACGACG 600

Qy    629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy    689 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy    749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTGGAGGACGTTAACGGGAAAGTGTGGAGG 808
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTGGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy    809 TTCCGGTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTCCGGTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy    869 TTCGTTAAGGAGGAAGAATCACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TTCGTTAAGGAGGAAGAATCACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy    929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy    989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCCGGAGAGTTCAAGAAACGACGTCGTA 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAAGATTTATCCGTTGGTGTGTAGCAAGAACAACGC 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAAGATTTATCCGTTGGTGTGTAGCAAGAACAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTTCTTTTGTTGTTTAATAATT 1168
          ||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTTTCTTTTGTTTGTTTTAATAATT 1139
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Db    841 TTCGTTAAGGAGGAAGAATCACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy    929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy    989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCCGGAGAGTTCAAGAAACGACGTCGTA 1048
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAAGAGTGAACGATACTGAAGATTTATCCGTTGGTGTGTAGCAAGAACAACGC 1108
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGAAACAAAAGAGTGAACGATACTGAAGATTTATCCGTTGGTGTGTAGCAAGAACAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTTCTTTTGTTTGTTTTAATAATT 1168
          ||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTTCTTTTGTTTGTTTTAATAATT 1139

Qy   1169 TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTTCTTCTTCTTCTTCTTGTTTACCAA 1228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1140 TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTTCTTCTTCTTCTTCTTGTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTGTGTATTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTGTGTATTGATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
          |||||||
Db   1260 TTAAAAA 1266
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RESULT 5
US-10-278-173-3
; Sequence 3, Application US/10278173
; Publication No. US20030061637A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Broun, Pierre
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Pineda, Omaira
; APPLICANT: Zhang, James
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Keddie, James
; APPLICANT: Heard, Jacqueline
; APPLICANT: Reuber, Lynne
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc
; APPLICANT: Samaha, Raymond
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION
; FILE REFERENCE: MBI-009
; CURRENT APPLICATION NUMBER: US/10/278,173
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G867
US-10-278-173-3

Query Match   95.9%; Score 1255; DB 14; Length 1281;
Best Local Similarity   99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy     29 CACAACACAAACACATTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT 88
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```

```
Qy   1169 TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTTCTTCTTCTTGTTTTACCAA 1228
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   1140 TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCGGTTTCTTCTTCTTGTTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTGTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 AGGTTCATGAGTTGTTTTGTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy   1289 TTAAAAA 1295
          |||||||
Db   1260 TTAAAAA 1266
```

RESULT 6

US-10-295-403-17

; Sequence 17, Application US/10295403
; Publication No. US20030101481A1
; GENERAL INFORMATION:
;   APPLICANT: Heard, Jacqueline
;   APPLICANT: Riechmann, Jose Luis
;   APPLICANT: Adam, Luc
;   APPLICANT: Broun, Pierre
;   APPLICANT: Pineda, Omaira
;   APPLICANT: Reuber, Lynne
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Keddie, James
;   APPLICANT: Zhang, James
;   APPLICANT: Benito, Maria-Ines
;   APPLICANT: Yu, Guo-Liang
;   APPLICANT: Fromm, Mike
;   TITLE OF INVENTION: PLANT GENE SEQUENCES I
;   FILE REFERENCE: MBI-0003
;   CURRENT APPLICATION NUMBER: US/10/295,403
;   CURRENT FILING DATE: 2002-11-15
;   PRIOR APPLICATION NUMBER: US/09/394,519
;   PRIOR FILING DATE: 1999-09-13
;   PRIOR APPLICATION NUMBER: 60/101,349
;   PRIOR FILING DATE: 1998-09-22
;   PRIOR APPLICATION NUMBER: 60/103,312
;   PRIOR FILING DATE: 1998-10-06
;   PRIOR APPLICATION NUMBER: 60/108,734
;   PRIOR FILING DATE: 1998-11-11
;   PRIOR APPLICATION NUMBER: 60/113,409
;   PRIOR FILING DATE: 1998-12-22
;   NUMBER OF SEQ ID NOS: 170
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 17
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)..(1095)
;   OTHER INFORMATION: G867

US-10-295-403-17

Query Match   95.9%; Score 1255; DB 15; Length 1281;
Best Local Similarity   99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy    29 CACACACAAACAACATTTCTGTTTTCCATTGTTTCAAACCATARAAAAAAAAACACAGAT 88
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACACACAAACAACATTTCTGTTTTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC 148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACACAGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGAGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
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Db   121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGAGGTAGGTAACTTATACAGGATGGGAAGCGGA 180
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Qy   509 TTGAGGAAACATACTTATATACGAAGAGTTAGAGCAGAGAGTAAACCGCTCGTAATGGTAAC 568
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATATACGAAGAGTTAGAGCAGAGAGTAAACCGCTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy   629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAG 688
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGACGTTGGGAG 808
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGACGTTGGGAG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
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Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGAAGAATCTACGTGCTCGTGTGACGTGGTTAGTTTCAGTGATCTAACGGT 928
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Db   841 TTCGTTAAGGAGAAGAATCTACGTGCTCGTGTGACGTGGTTAGTTTCAGTGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGGTGGAAGTGGAAGTCGAGATCCGGTCAGATTTAGATGCGGGGT 988
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGGTGGAAGTGGAAGTCGAGATCCGGTCAGATTTAGATGCGGGGT 960

Qy   989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAAGAGTGAACGATACTGAGAGATGTTATCGTGTGTGTAGCAAGAAGCAACGC 1108
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAAGAGTGAACGATACTGAGAGATGTTATCGTGTGTGTAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTTTCTTTGTGTTTTGTTTAATAATT 1168
             ||||||||||||||||||||||||||||||||||| -||||||||||||||||||||||
Db  1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTTTCTTTGTGTTTTGTTTAATAATT 1139

Qy  1169 TTTAAAAACTCCATTTCGTTTTCTTATTGCATCGGTTCCATCTGTGAAACC 1228
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTCCATTTCGTTTTCTTATTGCATCGGTTCCATCTGTGAAACC 1199

Qy  1229 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
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Db  1200 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
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Db  1260 TTAAAAA 1266
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RESULT 8
US-10-225-068-137
; Sequence 137, Application US/10225068
; Publication No. US20030217383A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Broun, Pierre E.

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Db  1260 TTAAAAA 1266
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RESULT 7
US-10-278-536-23
; Sequence 23, Application US/10278536
; Publication No. US20030131386A1
; GENERAL INFORMATION:
; APPLICANT: Samaha, Raymond
; APPLICANT: Heard, Jacqueline
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Pineda, Omaira
; APPLICANT: Reuber, Lynne
; APPLICANT: Riechmann, Jose-Luis
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Keddie, James
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pilgrim, Marsha
; APPLICANT: Adam, Luc
; APPLICANT: Broun, Pierre
; TITLE OF INVENTION: STRESS-INDUCED POLYNUCLEOTIDES
; FILE REFERENCE: MBI-011
; CURRENT APPLICATION NUMBER: US/10/278,536
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 23
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G867

US-10-278-536-23

Query Match   95.9%; Score 1255; DB 15; Length 1281;
Best Local Similarity 99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy   29 CACAACAAACAAACATTTCGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 88
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CACAACAAACAAACATTTCGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 148
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Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAGCGGA 208
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Db   121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAGCGGA 180

Qy   209 TCAAGCGTTGTGTTAGATTCAGAGAAGCGGCGTAGAAGCTGAATCGGAAGATGGGAGCTTCCGTCG 268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGATTCAGAGAAGCGGCGTAGAAGCTGAATCGGAAGATGGGAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAGCTTCAGATTACGAG 328
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Db   241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGATGGGAGCTTCAGATTACGAG 300

Qy   329 AAACACCAGCGCGTGTGGCTTCGGGACATTCAACGAAGAAGACGAAGCGCTTCGTGCCTAC 388
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCGTGTGGCTTCGGGACATTCAACGAAGAAGACGAAGCCGCTTCGTGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGAGCGCCGTCACAAATTTCAAAGACGTGAAG 448
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Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGAGCGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATTCTGATATCGTTGATATG 508
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Db   421 ATGGACGAAGACGAGGTCGATTTCTCATTCGAAATTCTGATATCGTTGATATG 480
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;   TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
;   TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
;   FILE REFERENCE: 51442002040
;   CURRENT APPLICATION NUMBER: US/10/225,068
;   CURRENT FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: 60/310,847
;   PRIOR FILING DATE: 2001-08-09
;   PRIOR APPLICATION NUMBER: 60/336,049
;   PRIOR FILING DATE: 2001-11-19
;   PRIOR APPLICATION NUMBER: 60/338,692
;   PRIOR FILING DATE: 2001-12-11
;   PRIOR APPLICATION NUMBER: 10/171,468
;   PRIOR FILING DATE: 2002-06-14
;   NUMBER OF SEQ ID NOS: 246
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 137
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1098)
US-10-225-068-137

Query Match  95.9%;  Score 1255;  DB 17;  Length 1281;
Best Local Similarity  99.9%;  Pred. No. 1.3e-281;
Matches 1266;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

Qy    29 CACAACACAAACACATTTCGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 88
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCGTTTCTCCATTGTTTCAAACCATAAAAAAAACACAGAT 60

Qy    89 TAAATGGAATCGAGTAGGCTTGATGAGTACTACACAGTTCCATCTGTGAAACC 148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGGCTTGATGAGTACTACACAGTTCCATCTCTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGTTGTGTTAGATTCAGAGAACGACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGATTCAGAGAACGACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGTGTGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAG 328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGTGTGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 388
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Db   301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC 360

Qy   389 GACGTCGGCGGTTCACAGGTTCCGTCGCCGTCGACGCCGTCACAAATTTCAAAGACGTGAAG 448
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGGCGGTTCACAGGTTCCGTCGCCGTCGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGACGAAGACGAGGTCGATTCTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 508
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGACGAAGACGAGGTCGATTCTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy   509 TTGAGGGAAACATACTTATAACGAAGAGAGTTAGACGCAGAGCTAAACGGCGTCGTAATGGTAAC 568
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGGAAACATACTTATAACGAAGAGAGTTAGACGCAGAGCTAAACGGCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 628
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG 600

Qy   629 GGGTTTAGATCGGCGGAGCACTGTTTGAGAAAGCGGTAACGGCCAAGCAGCGTTGGGAAG 688
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   601 GGGTTTAGATCGGCGGAGCACTGTTTGAGAAAGCGGTAACGCCCAAGCAGCGTTGGGAAG 660

Qy   689 CTAAACCGTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTGGTTATACCGAGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAGAAAGTGTGGAGG 808
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGAGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTTTGACTAAAGGTTCGGAGCAGG 868
         ||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTCGGAGCAGG 840

Qy   869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAAGAGTGAACGACTGAGATGTATCGTTGGTGGTGTGGTGAGCAAGAAGCAACGC 1108
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAAGAGTGAACGACTGAGATGTATCGTTGGTGGTGTGGTGAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCCGTAACAACTCCTCTCTTCTTTCTTTTTTTCTTTTGTTTGTTTAATAATT 1168
         ||||||||||||| |||||||||||||||| |||||| |||||||||||||||||||||||
Db  1081 ATCTTTCACGCCTCGTAACAACTCCTCTC-TTTTTTTCTTTTGTTTGTTTAATAATT 1139

Qy  1169 TTTAAAAACTCCATTTCGTTTTCTTATTGCATCGGTTTCTTCTTCTTGTTTACCAA 1228
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Db  1140 TTTAAAAACTCCATTTCGTTTTCTTATTGCATCGGTTTCTTCTTCTTGTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTGTTGTATTGATGAGAACTGTAAATTTATTTATAGGATAAATT 1288
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTGTTGTATTGATGAGAACTGTAAATTTATTTATAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
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Db  1260 TTAAAAA 1266
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RESULT 9
US-10-225-066A-795
;   Sequence 795, Application US/10/225,066A
;   Publication No. US20030226173A1
;   GENERAL INFORMATION:
;   APPLICANT: Mendel Biotechnology, Inc.
;   APPLICANT: RATCLIFFE, Oliver
;   APPLICANT: RIECHMANN, Jose Luis
;   APPLICANT: ADAM, Luc J
;   APPLICANT: DUBELL, Arnold T
;   APPLICANT: HEARD, Jacqueline E
;   APPLICANT: PILGRIM, Marsha L
;   APPLICANT: JIANG, Cai-zhong
;   APPLICANT: REUBER, T. Lynne
;   APPLICANT: CREELMAN, Robert A
;   APPLICANT: PINEDA, Omaira
;   APPLICANT: YU, Guo-Liang
;   APPLICANT: BROUN, Pierre E
;   TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
;   FILE REFERENCE: MBI0036-2 US
;   CURRENT APPLICATION NUMBER: US/10/225,066A
;   CURRENT FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: 09/837,444
;   PRIOR FILING DATE: 2001-04-18
;   PRIOR APPLICATION NUMBER: 60/310,847
;   PRIOR FILING DATE: 2001-08-09
;   PRIOR APPLICATION NUMBER: 60/336,049
;   PRIOR FILING DATE: 2001-12-05
;   PRIOR APPLICATION NUMBER: 60/338,692
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; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 795
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-795

Query Match     95.9%;   Score 1255;  DB 17;   Length 1281;
Best Local Similarity   99.9%;   Pred. No. 1.3e-281;
Matches 1266;   Conservative   0;   Mismatches   0;   Indels   1;   Gaps   1;

Qy         29 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 88
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Db          1 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGAT 60

Qy         89 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAGAGTACAGGTTCCATCTGTGAAACC 148
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TAAATGGAATCGAGTAGCGTTGATGAGTACTACAACTACACAGGTTCCATCTGTGAAACC 120

Qy        149 CCGGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
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Db        121 CCGGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy        209 TCAAGCGGTTGTGTTGATTCAGAGAACGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCAAGCGGTTGTGTTGATTCAGAGAACGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy        269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 300

Qy        329 AAACACCAGCGCGCCTGTGGCTCCGGACATTCAACGAAGAAGACGAAGCCGTCTGCGCCTAC 388
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACACCAGCGCGCCTGTGGCTCCGGACATTCAACGAAGAAGACGAAGCCGTCTGCGCCTAC 360

Qy        389 GACGTCGCGGTTCACAGTTCCGTCGCCGTCGACGCCGTCACAAATTTCAAAGACGTGAAG 448
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GACGTCGCGGTTCACAGTTCCGTCGCCGTCGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy        449 ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATG 508
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGATCGTTGATATG 480

Qy        509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy        569 GGAAACATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGAGTGGTTTCTACGACG 628
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGAAACATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGAGTGGTTTCTACGACG 600

Qy        629 GGGTTTAGATCGGCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGTTTAGATCGGCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCACGTTGGGAAG 660

Qy        689 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy        749 AACGTTTCCGTGAAAGGAGGAGTTGTTGTAACTTTGAGACTTTGACTAAAGGTTGGGAGG 808
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACGTTTCCGTGAAAGGAGGAGTTGTTGTAACTTTGAGACTTTGACTAAAGGTTGGGAGG 780

Qy        809 TTCCGTTACTCGTATTGGAACAGTACGTCGTCTGGTGACGTGGTTAGTTTCAGTAGTTGGA 868
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCGTTACTCGTATTGGAACAGTACGTCGTCTGGTGACGTGGTTAGTTTCAGTAGTTGGA 840

Qy        869 TTCGTTAAGGAGAAGAATCTACGTGCTCGGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCGTTAAGGAGAAGAATCTACGTGCTCGGTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy        929 CAGGATCAACAGTGTACATTGGGTGGAAGTCGAGATCGGGGTCAGATTTAGATGCGGGT 988
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CAGGATCAACAGTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy        989 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy       1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTCGTGTGGTGGTGTGTAGCAAGAAGCAACGC 1108
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTCGTGTGGTGGTGTGTAGCAAGAAGCAACGC 1080

Qy       1109 ATCTTTCACGCCCTCGTAACAACTCTCTCTTTTTTTTTTTGTGTTTGTTTTAATAATT 1168
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Db       1081 ATCTTTCACGCCCTCGTAACAACTCTCTC-TTTTTTTTTTTGTGTTTGTTTTAATAATT 1139

Qy       1169 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGGTTCTTCTTCTTCGTTGTTACCAA 1228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db       1140 TTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGGTTCTTCTTCTTCGTTGTTACCAA 1199

Qy       1229 AGGTTCATGAGTTGTTTTTGTTGTTGATTGATTGAACTGTAAATTTTATTTATAGGATAAAATT 1288
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1200 AGGTTCATGAGTTGTTTTTGTTGTTGATTGATTGAACTGTAAATTTTATTTATAGGATAAAATT 1259

Qy       1289 TTAAAAA 1295
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Db       1260 TTAAAAA 1266
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RESULT 10
US-10-374-780A-169
; Sequence 169, Application US/10374780A
; Publication No. US20040019927A1
; GENERAL INFORMATION:
;   APPLICANT: Sherman, Bradley K
;   APPLICANT: Riechmann, Jose Luis
;   APPLICANT: Jiang, Cai-Zhong
;   APPLICANT: Heard, Jacqueline E
;   APPLICANT: Haake, Volker
;   APPLICANT: Creelman, Robert A
;   APPLICANT: Ratcliffe, Oliver
;   APPLICANT: Adam, Luc J
;   APPLICANT: Reuber, T. Lynne
;   APPLICANT: Keddie, James
;   APPLICANT: Broun, Pierre B
;   APPLICANT: Pilgrim, Marsha L
;   APPLICANT: Dubell III, Arnold T
;   APPLICANT: Pineda, Omaira
;   APPLICANT: Yu, Guo-Liang
;   TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
;   FILE REFERENCE: MBI-0047 CIP
;   CURRENT APPLICATION NUMBER: US/10/374,780A
;   CURRENT FILING DATE:   2003-02-25
;   PRIOR APPLICATION NUMBER: 09/837,944
;   PRIOR FILING DATE: 2001-04-18
;   PRIOR APPLICATION NUMBER: 60/310,847
;   PRIOR FILING DATE: 2001-08-09
;   PRIOR APPLICATION NUMBER: 09/934,455
;   PRIOR FILING DATE: 2001-08-22
;   PRIOR APPLICATION NUMBER: 60/336,049
;   PRIOR FILING DATE: 2001-11-19
;   PRIOR APPLICATION NUMBER: 60/338,692
;   PRIOR FILING DATE: 2001-12-11
;   PRIOR APPLICATION NUMBER: 10/171,468
;   PRIOR FILING DATE: 2002-06-14
;   PRIOR APPLICATION NUMBER: 10/225,066
;   PRIOR FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: 10/225,067
;   PRIOR FILING DATE: 2002-08-09
;   PRIOR APPLICATION NUMBER: 10/225,068
;   PRIOR FILING DATE: 2002-08-09
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; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
;
; SEQ ID NO 169
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G867
US-10-374-780A-169

Query Match      95.9%;    Score 1255;  DB 17;    Length 1281;
Best Local Similarity   99.9%;    Pred. No. 1.3e-281;
Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    29 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT    88
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCTGTTTCTCCATTGTTTCAAACCATAAAAAAAAACACAGAT    60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACCAGGTTCCATCTGTGAAACC   148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACCAGGTTCCATCTGTGAAACC   120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCGGA   208
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Db   121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCGGA   180

Qy   209 TCAAGGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG   268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG   240

Qy   269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGAGATGGGGAGCTCAGATTTACGAG   328
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Db   241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAGAGATGGGGAGCTCAGATTTACGAG   300

Qy   329 AAACACCAGCGCGGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCGCTCGTGCCTAC   388
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Db   301 AAACACCAGCGCGGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCGCTCGTGCCTAC   360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCGTGACGCCGTCACAAATTTCAAAGACGTGAAG   448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCGTGACGCCGTCACAAATTTCAAAGACGTGAAG   420

Qy   449 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG   508
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATG   480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAAGACGCGGCCGCCGTCGTAATGGTAAC   568
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Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGAAGACGCGGCCGCCGTCGTAATGGTAAC   540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG   628
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACG   600

Qy   629 GGGTTTAGATCGGCCGGAGGCACTGTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAG   688
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Db   601 GGGTTTAGATCGGCCGGAGGCACTGTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAG   660

Qy   689 CTAAACCGTTTGGTTATACCGGAAACATCACGCGAGAAACATTTCCGTTACCGTCAAGT   748
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGGAAACATCACGCGAGAAACATTTCCGTTACCGTCAAGT   720

Qy   749 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTCGGAGG   808
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Db   721 AACGTTTCCGTGAAAGGAGTGTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTCGGAGG   780

Qy   809 TTCCGTTACTCCGTATTGGAACAGTAGTCGAGAGTTATGTTTCGACTAAAGGTTGGAGCAGG   868
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Db   781 TTCCGTTACTCCGTATTGGAACAGTAGTCGAGAGTTATGTTTCGACTAAAGGTTGGAGCAGG   840

Qy   869 TTCGTTAAGGAGAAGAATCTACGTGCGTGGTGACGTCGGTTAGTTTCAGTAGATCTAACGGT   928
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Db   841 TTCGTTAAGGAGAAGAATCTACGTGCGTGGTGACGTCGGTTAGTTTCAGTAGATCTAACGGT   900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT   988
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT   960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTA  1048
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA  1020

Qy  1049 GGAAACAAAAGATGAACGATACTGAGATGTATCGTGGTGGTGTAGCAGAAGCAACGC  1108
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAAGATGAACGATACTGAGATGTATCGTGGTGGTGTAGCAGAAGCAACGC  1080

Qy  1109 ATCTTTCACGCCTGTAACAACTCTCTTCTTTTTTTTTTTTTGTTGTTTAATAATT  1168
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Db  1081 ATCTTTCACGCCTGTAACAACTCTCTTCTTC-TTTTTTTTTTTTGTTGTTTTAATAATT  1139

Qy  1169 TTTAAAACTCCATTTTCGTTTTCTTATTTGCATCCGTTTCTTTCTTCTTGTTTACCAA  1228
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Db  1140 TTTAAAACTCCATTTTCGTTTTCTTATTTGCATCCGTTTCTTTCTTCTTGTTTACCAA  1199

Qy  1229 AGGTTCATGAGTTGTTTTGTTGTGTTATGATGAACTGTAAATTTTATTTATAGAGATAAATT  1288
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTGTTGTGTTATGATGAACTGTAAATTTTATTTATAGGATAAATT  1259

Qy  1289 TTAAAAA  1295
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Db  1260 TTAAAAA  1266
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;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/713,994
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 09/819,142
;  PRIOR FILING DATE: 2001-03-27
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 2011
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 579
;  LENGTH: 1281
;  TYPE: DNA
;  ORGANISM: Arabidopsis thaliana
;  FEATURE:
;  OTHER INFORMATION: G867
US-10-412-699B-579

  Query Match          95.9%;  Score 1255;  DB 18;  Length 1281;
  Best Local Similarity  99.9%;  Pred. No. 1.3e-281;
  Matches 1266;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy   29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAAAAACACAGAT 88
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Db    1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAAAAAACACAGAT 60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACACAGGTTCCATCTGTGAAACC 148
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Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACACAGGTTCCATCTGTGAAACC 120

Qy  149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGA 208
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Db  121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGA 180

Qy  209 TCAAGGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAAGCTTCCGTCG 268
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Db  181 TCAAGGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAAGCTTCCGTCG 240

Qy  269 TCAAAATACAAAGGTGTGTGCCACAACAACCGAAGATGGGAGACTTCAGATTTACGAG 328
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Db  241 TCAAAATACAAAGGTGTGTGCCACAACAACCGAAGATGGGAGACTTCAGATTTACGAG 300

Qy  329 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAAGCCGCTCGTGCCTAC 388
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Db  301 AAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAGACGAAGCCGCTCGTGCCTAC 360

Qy  389 GACGTCGCCGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG 448
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Db  361 GACGTCGCCGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTCAAAGACGTGAAG 420

Qy  449 ATGGACGAAGACGAGGTCGATTTCTTCGTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 508
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Db  421 ATGGACGAAGACGAGGTCGATTTCTTCGTGAATTCTCATTCGAAATCTGAGATCGTTGATATG 480

Qy  509 TTGAGGAAACATACTTATACAGAGAGTTAGACGAGGTAGAGCAGAGCGTCGTAATGGTAAC 568
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Db  481 TTGAGGAAACATACTTATACAGAGAGTTAGACGAGGTAGAGCAGAGCGTCGTAATGGTAAC 540

Qy  569 GGAAACATGACTAGGACGTGTTGTTAACGTCGGGGTTGAGTGATGGTGTTTCTACGACG 628
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Db  541 GGAAACATGACTAGGACGTGTTGTTAACGTCGGGGTTGAGTGATGGTGTTTCTACGACG 600

Qy  629 GGGTTTAGATCGGCCGAGGCACTGTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAG 688
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Db  601 GGGTTTAGATCGGCCGAGGCACTGTTGAGAAAGCCGTAACGCCAAGCGACGTTGGGAAG 660

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Qy  749 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
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Db  721 AACGTTTCCGTGAAAGGAGTGTGTTGTTGAACTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy  809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 868
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 840

Qy  869 TTCGTTAAGGAGGAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 928
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Db  841 TTCGTTAAGGAGGAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGT 900

Qy  929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCCGGGTCAGATTTAGATGCGGGT 988
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Qy  989 CGGGTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
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Db  961 CGGGTTTGAGATTGTTCCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy 1049 GGAAACAAAAGAGTGAACGATACTCGAGATGTATCGTTGGTGTGTAGCAAGAAGCAACGC 1108
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Db 1021 GGAAACAAAAGAGTGAACGATACTCGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGC 1080

Qy 1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTCTTTTGTGTGTTTTTAATAATT 1168
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Db 1081 ATCTTTCACGCCTCGTAACAACTCTTCTC-TTTTTTTTCTTTTGTGTGTTTTTAATAATT 1139

Qy 1169 TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTTCTTCTTTCGTTGTTACCAA 1228
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Db 1140 TTTAAAAACTCCATTTCGTTTCTTATTTGCATCGGTTTCTTCTTTCGTTGTTACCAA 1199

Qy 1229 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTATTTATTAGGATAAATT 1288
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Db 1200 AGGTTCATGAGTTGTTTTGTTGTATTGATGAACTGTAAATTTATTTATTAGGATAAATT 1259

Qy 1289 TTAAAAA 1295
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Db 1260 TTAAAAA 1266


RESULT 12
US-10-685-922-1
; Sequence 1, Application US/10685922
; Publication No. US20040098764A1
; GENERAL INFORMATION:
;  APPLICANT: MENDEL BIOTECHNOLOGY, INC.
;  APPLICANT: HEARD, Jacqueline
;  APPLICANT: RIECHMANN, Jose Luis
;  APPLICANT: CREELMAN, Robert
;  APPLICANT: RATCLIFFE, Oliver
;  APPLICANT: KUMIMOTO, Roderick W
;  APPLICANT: GUTTERSON, Neal
;  APPLICANT: REUBER, T Lynne
;  APPLICANT: PINEDA, Omaira
;  APPLICANT: LIBBY, Jeffrey M
;  APPLICANT: SHERMAN, Bradley K
;  TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF ABIOTIC STRESS
;  FILE REFERENCE: MBI-0049CIP
;  CURRENT APPLICATION NUMBER: US/10/685,922
;  CURRENT FILING DATE: 2003-10-14
;  PRIOR APPLICATION NUMBER: 09/810,836
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 10/412,699
;  PRIOR FILING DATE: 2003-04-10
;  PRIOR APPLICATION NUMBER: 10/171,468
;  PRIOR FILING DATE: 2002-06-14
;  PRIOR APPLICATION NUMBER: 09/532,591
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/533,029
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 09/533,392
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: 60/125,814
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: 09/713,994
;  PRIOR FILING DATE: 2000-11-16
;  PRIOR APPLICATION NUMBER: 60/166,228
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; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/394,519
; PRIOR FILING DATE: 1999-09-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G867 Predicted polypeptide sequence is paralogous to G9, G993, G1
US-10-685-922-1

Query Match   95.9%; Score 1255; DB 18; Length 1281;
Best Local Similarity 99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy   29 CACAACAAACACATTCTGTTTCTCCATTGTTCAAACCATAAAAAAAACACAGAT   88
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CACAACAAACACATTCTGTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGAT   60

Qy   89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACACAGGTTCCATCTGTGAAACC 148
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Db   61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAGTACACAGGTTCCATCTGTGAAACC 120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACACGGATGGGAAGCGGA 208
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACACGGATGGGAAGCGGA 180

Qy   209 TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 268
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 328
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGTGTGTGCCACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGCGTGTGCTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTCGTGCCTAC 388
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Db   301 AAACACCAGCGCGCGTGTGCTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTCGTGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
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Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACCAGGTCGATTTCTTGAATTCCATTCGAAATCTGAGATCGTTGATATG 508
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Db   421 ATGGACGAAGACGAGGTCGATTTCTTGAATTCCATTCGAAATCTGAGATCGTTGATATG 480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAATGGTAAC 568
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTGAATGATGGTGTTCTACGACG 628
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTGAATGATGGTGTTCTACGACG 600

Qy   629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTTGGTTATACCGACAATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGACAATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGAGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGAGAGTGTGTTGTTGAACTTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 868
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTGGTCAGTAGATCTAACGGT 928
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGGAAGAATCTACGTGCGTGGTGGTCAGTAGATCTAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTTGAGATTGTTCGGAGTAACATTCACCGGAGAAGTCAAGAAACGACGTCGTA 1048
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTTGAGATTGTTCGGAGTAACATTCACCGGAGAAGTCAAGAAACGACGTCGTA 1020

Qy 1049 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGAGCAAGAAGCACGC 1108
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 GGAAACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTGAGCAAGAAGCAAGC 1080

Qy 1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTCTTTGTTTGTTTAATAATT 1168
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db 1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC-TTTTTTTCTTTGTTTGTTTAATAATT 1139

Qy 1169 TTTAAAACTCCATTTTCGTTTTCGTTTTCTTATTTGCATCGTTTCTTCTTTGTTTACCAA 1228
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1140 TTTAAAACTCCATTTTCGTTTTCGTTTTCTTATTTGCATCGTTTCTTCTTTGTTTACCAA 1199

Qy 1229 AGGTTCATGAGTTGTTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1200 AGGTTCATGAGTTGTTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259

Qy 1289 TTAAAAA 1295
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Db 1260 TTAAAAA 1266

RESULT 13
US-10-225-068-137
; Sequence 137, Application US/10225068
; Publication No. US20050120408A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Heard, Jacqueline E.
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Adam, Luc J.
; APPLICANT: Dubell, Arnold T.
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Pineda, Omaira
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Broun, Pierre E.
; TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
; TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
; FILE REFERENCE: 51444002040
; CURRENT APPLICATION NUMBER: US/10/225,068
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1098)
US-10-225-068-137

Query Match   95.9%; Score 1255; DB 21; Length 1281;
Best Local Similarity   99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy    29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATCAAAAAAAACACAGAT   88
         |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATCAAAAAAAACACAGAT   60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  120

Qy   149 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA  208
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA  180

Qy   209 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  268
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCAAGCGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCG  240

Qy   269 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTTCAGATTTACGAG  328
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TCAAAATACAAAGGTGTGGTGCCACAACCAAACGGAAGATGGGGAGCTTCAGATTTACGAG  300

Qy   329 AAACACCAGCGCGTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC  388
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AAACACCAGCGCGTGTGGCTCGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTAC  360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTTCAAAGACGTGAAG  448
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTTCAAAGACGTGAAG  420

Qy   449 ATGACGAAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  508
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGACGAAGACGAGGTCGATTTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATG  480

Qy   509 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACCGGCGTCGTAATGGTAAC  568
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACCGGCGTCGTAATGGTAAC  540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCACGACG  628
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCACGACG  600

Qy   629 GGGTTAGATCGGCGGAGGCACTCGTTGAGAAAGCGGTAACGCCAAGCGACGCGTTGGGAAG  688
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GGGTTAGATCGGCGGAGGCACTCGTTGAGAAAGCGGTAACGCCAAGCGACGCGTTGGGAAG  660

Qy   689 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  748
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTAAACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT  720

Qy   749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTGACGGGAAAGTGTGGAGG  808
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTGACGGGAAAGTGTGGAGG  780

Qy   809 TTCCGTTACTCGTATTCGGAACAGTTGGAACAGTAGTCAGAGTTATGTTTT  868
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TTCCGTTACTCGTATTCGGAACAGTTGGAACAGTAGTCAGAGTTATGTTTT  840

Qy   869 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGTCGTTGGTTAGTTCAGTATCTAACGGT  928
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTCGTTAAGGAGAAGAATCTACGTGCTGGTGTCGTTGGTTAGTTCAGTATCTAACGGT  900

Qy   929 CAGGATCAACAGTTGTACATTTGGGTGGAAGTCGAGATCGGGTCAGATTTAGATGCGGGT  988
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CAGGATCAACAGTTGTACATTTGGGTGGAAGTCGAGATCGGGTCAGATTTAGATGCGGGT  960

Qy   989 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CGGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy  1049 GGAAACAAAAGAGTGAACCATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1108
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 GGAAACAAAAGAGTGAACCATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1080

Qy  1109 ATCTTTCACGCCTCGTAACAACTCTCTTCCTTTTTTTTTCTTTTGTTGTTTGTTTAATAATT 1168
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  1081 ATCTTTCACGCCTCGTAACAACTCTCTC-TTTTTTTTTCTTTTGTTGTTTGTTTAATAATT 1139

Qy  1169 TTTAAAAACTCCATTTTCGTTTCTTATTTGCATCGGTTTCTTCTTTCTTGTTTACCAA 1228
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1140 TTTAAAAACTCCATTTTCGTTTCTTATTTGCATCGGTTTCTTCTTTCTTGTTTACCAA 1199

Qy  1229 AGGTTCATGAGTTGTTTTTGTTGTTATTGATGAACTGTAAATTTTATTTATTAGGATAAATT 1288
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1200 AGGTTCATGAGTTGTTTTTGTTGTTATTGATGAACTGTAAATTTTATTTATTAGGATAAATT 1259

Qy  1289 TTAAAAA 1295
         |||||||
Db  1260 TTAAAAA 1266
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RESULT 14
US-10-225-066A-795
; Sequence 795, Application US/10225066A
; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omaira
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MBI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 795
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-795

Query Match   95.9%; Score 1255; DB 22; Length 1281;
Best Local Similarity   99.9%; Pred. No. 1.3e-281;
Matches 1266; Conservative   0; Mismatches   0; Indels   1; Gaps   1;

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Qy    29 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATCAAAAAAAACACAGAT   88
         |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     1 CACAACACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATCAAAAAAAACACAGAT   60

Qy    89 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  148
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TAAATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACC  120
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Db   1200 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1259
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Qy   1289 TTAAAAA 1295
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          |||||||
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Db   1260 TTAAAAA 1266

RESULT 15
US-09-938-842A-2316
; Sequence 2316, Application US/09938842A
; Patent No. US2002016037BA1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2316
; LENGTH: 1035
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2316

Query Match   79.1%;   Score 1035;   DB 9;   Length 1035;
Best Local Similarity   100.0%;   Pred. No. 1.9e-230;
Matches 1035;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   92 ATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCG 151
```
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   1 ATGGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCG 60

Qy   152 GCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA 211
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   61 GCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGATCA 120

Qy   212 AGGCTTGTGTTAGATTCAGAGAACGGCGTAGGAGCTAGGAAGCTTCCGTCGTCA 271
```
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   121 AGGCTTGTGTTAGATTCAGAGAACGGCGTAGGAGCTAGGAAGCTTCCGTCGTCA 180

Qy   272 AAATACAAAGGTGGTGCCACAACCAAACGAAGAAGATGGGAGACGAAGCCGCTACGAC 331
```
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   181 AAATACAAAGGTGGTGCCACAACCAAACGAAGAAGATGGGAGACGAAGCCGCTACGAC 240

Qy   332 CACCAGCGCGTGTGGCTCGGGACATTCAACGAAGCCGCTCACAAATTTCAAAGACGTGAAGATG 391
```
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   241 CACCAGCGCGTGTGGCTCGGGACATTCAACGAAGCCGCTCACAAATTTCAAAGACGTGAAGATG 300

Qy   392 GTGCGGGTTCACAGGTTCCGTCGCGGAGTTCTTGAATTCTCATTCGAAATCTGAAATCTGAAATCTGAAATGTTG 451
```
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   301 GTGCGGGTTCACAGGTTCCGTCGCGGAGTTCTTGAATTCTCATTCGAAATCTGAAATCTGAAATGTTG 360

Qy   452 GACGAAGACGAGGTCGATTTCATTCGAAATCTGAAATCTGAAATCGTTGATATGTTG 511
```
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   361 GACGAAGACGAGGTCGATTTCATTCGAAATCTGAAATCGTTGATATGTTG 420

Qy   512 AGGAAACATACTTATACCAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGAA 571
```
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   421 AGGAAACATACTTATACCAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGAA 480

Qy   572 AACATGACTAGGACGTTGTAACGTCGGGGTTGATGAATGATGGTGTTCTACGACGGG 631
```
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   149 CCGGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 208
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   121 CCGGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGGAAGCGGA 180

Qy   209 TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAGCTGAATCTAGGAAGCTTCCGTCG 268
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   181 TCAAGCGGTTGTGTTAGATTCAGAGAACGGCGTAGAGCTGAATCTAGGAAGCTTCCGTCG 240

Qy   269 TCAAAATACAAAGGTGGTGTGCCACAACCAAACGAAGATGGGAGCTCAGATTTACGAG 328
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   241 TCAAAATACAAAGGTGTGTGCCACAACCAAACGGAGATGGGAGCTCAGATTTACGAG 300

Qy   329 AAACACCAGCGCGTGCTGCGGGACATTCAACGAAGAAGACGAAGAGCCGCTCGTGCCTAC 388
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   301 AAACACCAGCGCGTGCTGCGGGACATTCAACGAAGAAGACGAAGAGCCGCTCGTGCCTAC 360

Qy   389 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 448
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   361 GACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAG 420

Qy   449 ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGAATCTGATCGTTGATATG 508
```
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   421 ATGGACGAAGACGAGGTCGATTTCTTCATTCGAAATCTGAGAATCTGATCGTTGATATG 480

Qy   509 TTGAGGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 568
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   481 TTGAGGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAC 540

Qy   569 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG 628
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   541 GGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACG 600

Qy   629 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 688
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   601 GGGTTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAG 660

Qy   689 CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 748
```
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   661 CTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGT 720

Qy   749 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTGAGGACGTTAACGGGAAAGTGTGGAGG 808
```
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   721 AACGTTTCCGTGAAAGGAGTGTTGTTGAACTTGAGGACGTTAACGGGAAAGTGTGGAGG 780

Qy   809 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 868
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   781 TTCCGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTGACTAAAGGTTGGAGCAGG 840

Qy   869 TTCGTTAAGGAAGAATCTACGTGCTGGTAGTTCAGATCTTAAGGTTAGTTCAGTAGATCTAAACGGT 928
```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   841 TTCGTTAAGGAAGAATCTACGTGCTGGTAGTTCAGATCTTAAGGTTAGTTCAGTAGATCTAAACGGT 900

Qy   929 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 988
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```
Db   901 CAGGATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGT 960

Qy   989 CGGGTTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   961 CGGGTTTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1020

Qy   1049 GGAAACAAAGAGTGGAACGATACTGAGATGTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1108
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1021 GGAAACAAAGAGTGGAACGATACTGAGATGTATCGTTGGTGTGTGTAGCAAGAAGCAACGC 1080

Qy   1109 ATCTTTCACGCCTCGTAACAACTCTTCTTCTGTTTTTGTTTTGTTTTCTTTTGTTTTAATAATT 1168
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           |||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
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Db   1081 ATCTTTCACGCCTCGTAACAACTCTTCTTC---TTTTTTTTGTTTTCTTTTGTTTTTAATAATT 1139

Qy   1169 TTTAAAAACTCCATTTCGTTTCTTTATTTGCATCCGGTTTCTTTTCTTTCTTTGTTTACCAA 1228
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           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1140 TTTAAAAACTCCATTTCCATTTCGTTTCTTTTTTGCATCCGGTTTCTTTTCTTTCTTTGTTTTACCAA 1199

Qy   1229 AGGTTCATGAGTTGTTTTGTGTATTGATGAACTGTAAATTTTATTTATAGGATAAATT 1288
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Db    481 AACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGG 540

Qy    632 TTTAGATCGGCGGAGGCACTGTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTA 691
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Qy    692 AACCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAAC 751
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Qy    752 GTTTCCGTGAAAGGAGTGTGTTGTTGAACTTGAGGACGTTAACGGGAAAGTGTGGAGGTTC 811
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Qy    812 CGTTACTCGTATTGGAACAGTAGTCAGAGTTATGTTTTGACTAAAGGTTGGAGCAGGTTC 871
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    872 GTTAAGGAGAAGAATCTACGTGCTCGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAG 931
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Db    781 GTTAAGGAGGAAGAATCTACGTGCTCGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAG 840

Qy    932 GATCAACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGG 991
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Db    841 GATCAACACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGG 900

Qy    992 GTTTTGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTTCGTAGGA 1051
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Qy   1052 AACAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGCATC 1111
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Qy   1112 TTTCACGCCTCGTAA 1126
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Search completed: September 11, 2005, 09:20:56
Job time : 1005.55 secs

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OM nucleic - nucleic search, using sw model

                 GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:        September 11, 2005, 00:07:40 ; Search time 4991.21 Seconds
                                    (without alignments)
                                    9975.140 Million cell updates/sec

Title:         US-10-632-436A-1
Perfect score: 1308
Sequence:      1 gtatacatatacacacacata........ttaaaaagggttacttagat 1308
Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
Searched:      34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:     68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
               1: gb_est1:*
               2: gb_est2:*
               3: gb_htc:*
               4: gb_est3:*
               5: gb_est4:*
               6: gb_est5:*
               7: gb_est6:*
               8: gb_gss1:*
               9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES
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Result No.	Score	Query Match %	Length	DB	ID	Description
1	1261.4	96.4	1275	3	CNS0AAHR	BX817019 Arabidops
2	1226.8	93.8	1397	3	CNS0ABBS	BX815799 Arabidops
3	1179.4	90.2	1309	3	CNS0ABRD	BX816625 Arabidops
4	1157.6	88.5	1391	3	CNS0ABP0	BX816249 Arabidops
5	1108.6	84.8	1387	3	CNS09YIT	BX841829 Arabidops
6	670.2	51.3	704	5	BU635864	BU635864 039F02 In
7	612.6	46.8	1048	6	CB686050	CB686050 Bn01b 03b
8	566	43.3	586	6	CB257063	CB257063 47-E01274
9	534	40.8	534	1	AV527557	AV527557 AV527557
10	518.6	39.6	752	5	BU238054	BU238054 D801.14g0
11	504	38.5	504	1	AV537025	AV537025 AV537025
c 12	503.8	38.5	546	1	AV439943	AV439943 AV439943
c 13	493.4	37.8	969	8	BZ458719	BZ458719 BONKU85TF
14	493.4	37.7	860	9	AJ597800	AJ597800 Arabidops
15	478.4	36.6	480	1	AI994740	AI994740 701499474
16	465.4	35.6	467	1	AV519075	AV519075 AV519075
c 17	423.4	32.4	425	1	AV788518	AV788518 AV788518
c 18	409.6	31.3	428	5	BP606510	BP606510 BP606510
19	406.2	31.1	575	7	N37328	N37328 18555 Lambd
c 20	404	30.9	415	8	BZ768017	BZ768017 SALK_1396
c 21	401.8	30.7	440	1	BP620288	BP620288 BP620288
c 22	398.4	30.5	412	1	AV789688	AV789688 AV789688
c 23	395	30.2	418	5	BP608988	BP608988 BP608988
c 24	384	29.4	420	5	BP612748	BP612748 BP612748
c 25	378.8	29.0	428	1	AV800762	AV800762 AV800762
c 26	375.2	28.7	464	3	BP609612	BP609612 BP609612
27	371.8	28.4	1304	3	CNS0ABR3	BX816580 Arabidops
c 28		27.2	421	8	BP643459	BP643459 SALK_0218
c 29	346.2	26.5	434	8	BZ288479	BZ288479 SALK_0218
c 30	341	26.1	371	5	BP602903	BP602903 BP602903
31	338.4	25.9	345	5	BP561325	BP561325 BP561325
32	338	25.8	484	7	T43470	T43470 6733 Lambda
c 33	296	22.6	825	8	BZ469001	BZ469001 BONIN92TF
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35	294.8	22.5	315	1	AV520986	AV520986 AV520986
36	290.6	22.2	450	7	N37218	N37218 18428 Lambd
37	288.4	22.0	945	3	CNS0ABW6	BX815867 Arabidops
38	277	21.2	277	7	Z37232	Z37232 ATTS3975 AC
c 39	277	21.2	433	5	BP633826	BP633826 BP63382G
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41	272.8	20.9	897	7	CK263261	CK263261 EST709339
42	270.6	20.7	756	5	BU636754	BU636754 011C04 In
c 43	270.4	20.7	429	5	BP605529	BP605529 BP605529
44	269.4	20.6	756	5	BQ971511	BQ971511 QHB7E05.y
45	268.2	20.5	743	5	BU025988	BU025988 QHG12J17.

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                                    ALIGNMENTS

RESULT 1
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LOCUS       CNS0AAHR               1275 bp    mRNA     linear   HTC 06-FEB-2004
DEFINITION  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
            GSLTPGH81ZA05 of Hormone Treated Callus of strain col-0 of
            Arabidopsis thaliana (thale cress).
ACCESSION   BX817019
VERSION     BX817019.1  GI:4247000I
KEYWORDS    HTC; GSLT cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1275)
  AUTHORS   Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
            Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
  TITLE     Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
            A Combined Approach to Evaluate and Improve Arabidopsis Genome
            Annotation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1275)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            Life Technologies (a division of Invitrogen) members carried out
            full-length librairies construction : Temple G.
            Genoscope members carried out sequencing and annotation: Castelli
            V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
            Schachter V., Weissenbach J., Salanoubat M.
            URGV INRA : Clepet C., Caboche M.
            Annotation is based on the June 2003 version of the Arabidopsis
            genome released by MIPS (Munich Information center for Protein
            Sequences). 5 prime and 3 prime are assembled with Phrap.
            http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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Best Local Similarity 99.8%;  Pred. No. 3.5e-283;
Matches 1273;  Conservative 0;  Mismatches 1;  Indels 1;  Gaps 1;

Qy       34 CACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAACACAGATTAAAT  93
            |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        1 CACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAACACAGATTAAAT  60

Qy       94 GGAATCGAGTAGCGTTGATGAGAGTACTACACAAGTTCCATCTGTGAAACCCCGGC  153
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GGAATCGAGTAGCGTTGATGAGAGTACTACACAAGTTCCATCTGTGAAACCCCGGC  120

Qy      154 GATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCCGATCAAG  213
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GATAACTCCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGAAGCCGATCAAG  180

Qy      214 CGTTGTGTTAGATTCAGAGAACGACGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA  273
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 CGTTGTGTTAGATTCAGAGAACGACGCGTAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA  240

Qy      274 ATACAAAGGTGTGGTGCCACAACCCAAACGAAGAATGGGAGCTCAGATTTACGAGAGAAACA  333
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 ATACAAAGGTGTGGTGCCACAACCCAAACGAAGAATGGGAGCTCAGATTTACGAGAGAAACA  300

Qy      334 CCAGCGCGTGGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTCGTCCTACGACGT  393
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy      394 CGCGGTTCACAGGTTCCGTGACGCCGTCACAAATTTCAAAGACGTGAAGATGGA  453
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Qy      454 CGAAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGAATCTGAGATCGTTGATATGTTGAG  513
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Db      421 CGAAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGAATCTGAGATCGTTGATATGTTGAG  480

Qy      514 GAAACATACTTATAAACGAAGAGTTAGAGCAGCAGAGTAAACGGCCGTCGTAATGGTAACGGAAA  573
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Qy      574 CATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGCGGGGTT  633
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Qy      634 TAGAATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAGCTAAA  693
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Db      601 TAGAATCGGCGGAGGCACTGTTTGAGAAAGCGTAACGCCAAGCGACGTTGGGAAGCTAAA  660

Qy      694 CCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAACGT  753
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Qy      754 TTCCGTGAAAAGAGAGTGTGTTGAACTTTGTTGAAGACGTTAACGGGAAAGTGTGGAGGTTCCG  813
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Qy      814 TTACTCGTATTGGAACAGTAGCAGTTATGTTTGACTAAAGGTTGGACTAAAGGTTCGT  873
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Qy      874 TAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGA  933
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Db      841 TAAGGAGAAGAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTAACGGTCAGGA  900

Qy      934 TCAACAGTTGTACATTGGGTGGAAGTCGAGATCGCGGGTCAGATTTAGATGCGGGTCGGGT  993
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Db      901 TCAACAGTTGTACATTGGGTGGAAGTCGAGATCGCGGGTCAGATTTAGATGCGGGTCGGGT  960

Qy      994 TTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTAGGAAA  1053
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Qy     1054 CAAAAGAGTGAACGATACTGAGATGTTATCGTTGGTGGTGTAGCAAGAAGCAACGCCATCTT  1113
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Qy     1114 TCACGCCTCGTA-ACAACTCTCTTCTTCTTTTGTGTTTTAATAATTTTA  1172
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Qy     1173 AAAACTCCATTTCGTTTTCTTTATTGCATCGGTTCTTTCTTCTTCTTGTTTACCAAAGGT  1232
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Qy     1293 AAAGGGTTACTTAGA  1307
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Db     1261 AAAGGGTTACTTAGA  1275
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RESULT 2
CNS0ABBS
LOCUS           CNS0ABBS                1397 bp    mRNA    linear    HTC    06-FEB-2004
DEFINITION      Arabidopsis thaliana Full-length cDNA Complete sequence from clone
                GSLTLS9ZE03 of Adult vegetative tissue of strain col-0 of
                Arabidopsis thaliana (thale cress).
ACCESSION       BX815799
VERSION         BX815799.1  GI:42470960
KEYWORDS        HTC; GSLT cDNA.
SOURCE          Arabidopsis thaliana (thale cress)
  ORGANISM      Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE       1  (bases 1 to 1397)
  AUTHORS       Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
                Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
                Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
  TITLE         Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
                A Combined Approach to Evaluate and Improve Arabidopsis Genome
                Annotation
  JOURNAL       Unpublished
REFERENCE       2  (bases 1 to 1397)
  AUTHORS       Genoscope.
  TITLE         Direct Submission
  JOURNAL       Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT         The sequences are based on single pass reads.
                Life Technologies (a division of Invitrogen) members carried out
                full-length librairies construction : Temple G.
                Genoscope members carried out sequencing and annotation : Castelli
                V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
                Schachter V., Clepet C., Caboche M.
                URGV INRA : Clepet C., Caboche M.
                Annotation is based on the June 2003 version of the Arabidopsis
                genome released by MIPS (Munich Information center for Protein
                Sequences). 5 prime and 3 prime are assembled with Phrap.
                http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                http://www.genoscope.cns.fr/cgi-bin/cgi-bin/ggb/ggb?source=Arabidopsis.
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Qy  111 ATGAGAGTACTACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAA 170
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Qy  171 AGTCGTCGGTAGTAACTTATACAGGATGGGAAGCGGATCAAGCGGTTGTGTTAGATTCAG 230
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Qy  231 AGAACGGCGTAGGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGGTGC 290
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Qy  291 CACAACCAAACGGAAGATGGGGAGCTCAGATTTACGAGAAACACCAGCGGCGTGGGCTCG 350
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Qy  351 GGACATTCAACGAAGAAGACGAAGCCGCTCGTCGTCCTACGACGTCGCGGTTCACAGGTTCC 410
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Qy  411 GTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGAGAGGTCGATT 470
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Qy  471 TCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATACG 530
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Qy  531 AAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAGTAACGGAAACATGACTAGGACGTTGT 590
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Db  481 AAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAAGTAACGGAAACATGACTAGGACGTTGT 540

Qy  591 TAACGTCGGGGTTGAGTAATGATGTGTTCTACGACGGGGTTTAGATCGGCGGAGGCAC 650
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Db  541 TAACGTCGGGGTTGAGTAATGATGTGTTCTACGACGGGGTTTAGATCGGCGGAGGCAC 600

Qy  651 TGTTTGAGAAAGCCGGTAAACGCGTAAGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGA 710
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Db  601 TGTTTGAGAAAGCCGGTAAACGCGTAAGCCAAGCGACGTTGGGAAGCTAAACCGTTTGGTTATACCGA 660

Qy  711 AACATCACGCAGAGAAACATTTCCGTTACCGTCAAGTAACGTTCCGTGAAAGGAGTGT 770
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Db  661 AACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTTCCGTGAAAGGAGTGT 720

Qy  771 TGTTGAACTTGAGGACGTTAACGGCGAAAGTGTGAGGTTCCGTTACTCCGTATTGGAACA 830
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 TGTTGAACTTGAGGACGTGGTTAGTTCAGTTCAGATCAACGGTCAACAGTTGTACATTG 780

Qy  831 GTAGTCAGAGTATGTTTGACTAAAGGTTGGACCAGGTTCGTTAAGGAGAAGAATCTAC 890
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 GTAGTCAGAGTATGTTTGACTAAAGGTTGGACCAGGTTCGTTAAGGAGAAGAATCTAC 840

Qy  891 GTGCTGGTGACGTGGTTAGTTTCAGTTCAGATCAACGGTCAACAGTTGTACATTG 950
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GTGCTGGTGACGTGGTTAGTTTCAGTTCAGATCAACGGTCAACAGTTGTACATTG 900

Qy  951 GGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGGGTTTGAGATTGTTCGGAG 1010
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GGTGGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGGGTTTGAGATTGTTCGGAG 960

Qy 1011 TTAACATTTCACCGGAGAGTTCAAGAAACGACGACGTCGTAGGAACAAAAGAGTGAACGATA 1070
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Db  961 TTAACATTTCACCGGAGAGTTCAAGAAACGACGACGTCGTAGGAACAAAAGAGTGAACGATA 1020

Qy 1071 CTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTCACGCGCTCGTAACAAC 1130
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Db 1021 CTGAGATGTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTCACGCGCTCGTAACAAC 1080

Qy 1131 TCTTCTTCTTTTTTTTCGTTGTTTTTGTGTTTAATAATTTTTAATAAATTTTCGTTT 1190
        |||||||||  || ||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TCTTCTTTC-TTCCTTTTGTTGTTTTTGTGTTTAATAATTCTTAAAAACTCCATTTTCGTTT 1139

Qy 1191 TCTTTATTTGCATCGGTTTCTTCTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTTTGTT 1250
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Db 1140 TCTTTATTTGCATCGGTTTCTTCTTCTTGTTTACCAAAGGTTCATGAGTTGTCTTTTTGTT 1199

Qy 1251 GTATTGATGAACTGTAAATTTTATTTATTTATAGGATAAATTTTAAAAAGGGTTACTTAGAT 1308
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Db 1200 GTATTGATGAACTGTAAATCTCATTTATAGGATAAATCTTAAAAAGGGTTACTTAGAT 1257

RESULT 3
CNS0ABRD
LOCUS      CNS0ABRD     1309 bp    mRNA    linear    HTC   06-FEB-2004
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone
           GSLTPGH59ZE10 of Hormone Treated Callus of strain col-0 of
           Arabidopsis thaliana (thale cress).
ACCESSION  BX816625
VERSION    BX816625.1    GI:42471700
KEYWORDS   HTC; GSLT_cDNA.
SOURCE     Arabidopsis thaliana (thale cress)
  ORGANISM Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1  (bases 1 to 1309)
AUTHORS    Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
           Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
           Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE      Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
           A Combined Approach to Evaluate and Improve Arabidopsis Genome
           Annotation
JOURNAL    Unpublished
REFERENCE  2  (bases 1 to 1309)
AUTHORS    Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Menard,M., Cruaud,C.,
           Schachter V., Weissenbach J., Salanoubat M.
           URGV INRA : Clepet C., Caboche M.
TITLE      Direct Submission
JOURNAL    Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
           - Web : www.genoscope.cns.fr)
COMMENT    The sequences are based on single pass reads.
           Life Technologies (a division of Invitrogen) members carried out
           full-length librairies construction : Temple G.
           Genoscope members carried out sequencing and annotation : Castelli
           V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
           Schachter V., Weissenbach J., Salanoubat M.
           Annotation is based on the June 2003 version of the Arabidopsis
           genome released by MIPS (Munich Information center for Protein
           Sequences). 5 prime and 3 prime are assembled with Phrap.
           http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
           length
           http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
FEATURES             Location/Qualifiers
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                     /clone="GSLTPGH59ZE10"
                     /tissue_type="Hormone Treated Callus"
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gene            /plasmid="pCMVSPORT_6_"
                1..1309
                /gene="At1g13260"
ORIGIN

Query Match     90.2%;   Score 1179.4;  DB 3;  Length 1309;
Best Local Similarity   96.2%;   Pred. No. 4.5e-264;
Matches 1232;   Conservative  0;   Mismatches 41;   Indels  8;   Gaps  2;

Qy   36  CAAACACATTCCGTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGATTAAATGG   95
         |||||||||| ||||||||||||||||||||||||||    |||||||||||||||||
Db    1  CAAACACATTCTGTTTCTCCATTGTTCAAACCATAAGGAAAAACACAGATTAAATGG   60

Qy   96  AATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGAGTTCCATCGTGAAACCCCGGCGA  155
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Db   61  AATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGAGTTCCATCGTGAGACCCCGGCGA  120

Qy  156  TAACTCCGGCGAAAAAGTCGTCGTGAGTAGTAACTTATACAGGATGGGAAGCCGGATCAAGCG  215
         |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  TAACTCCCGGCGAAAGAGTCGTCGTGAGTAGTAACTTATACAGGATGGGAAGCCGGATCAAGCG  180

Qy  216  TTGTGTTAGATTCAGAGAACGACGGCGTAGGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAAT  275
         |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  181  TTGTGTTAGATTCAGAGAACGGCGGCGTAGGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAAT  240

Qy  276  ACAAAGGTGTGGTGCCACAACCAAACGAAGAGATGGGAGCTCAGATTTACGAGAAACACC  335
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Db  241  ACAAAGGTGTGGTGCCACAACCAAACGAAGAGATGGGAGCTCAGATTTACGAGAAACACC  300

Qy  336  AGCGCGTGTGGCGTCGGAGCATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCG  395
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Db  301  AGCGCGTGTGGCGTCGGAGCATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGTCG  360

Qy  396  CGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAGACGTGAAGATGACG  455
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Db  361  CGGTTCACAGGTTCCGTCGCCGTCAACGCCGTCACAAATTCAAAGACGTGAAGATGACG  420

Qy  456  AAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGA  515
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Db  421  AAGACGAGGTCGATTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGGA  480

Qy  516  AACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGGTAACGGAAACA  575
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Db  481  AACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCCTAATGGTAACGGAAACA  540

Qy  576  TGACTAGGACGGTTGTTAACGTGCGGGGTTGAGTAATGATGATGGTGTTTCTACGACGGGGGTTA  635
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Db  541  TGACTAGGACGGTTGTTAACGTGCGGGGTTGAGTAATGATGATGGTGTTTCTACGACGGGGGTTA  600

Qy  636  GATCGGCCGGAGCCACTCGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACC  695
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Db  601  GATCGGCCGGAGCCACTTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACC  660

Qy  696  GTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTT  755
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Db  661  GTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTTT  720

Qy  756  CCGTGAAAGGAGTGGTTGTGTGAACTTGGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTT  815
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Db  721  CCGTGAAAGGAGTGGTTGTGTGAACTTGGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTT  780

Qy  816  ACTCGTATTGGAACAGTAGTCAGAGTTTGACTAAAGGTTGACTCGTTA  875
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Db  781  ACTCGTATTGGAACAGTAGTCAGAGTTTGACTAAAGGTTGACTCGTTA  840

Qy  876  AGGAGAAGAAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTTAACGGTCAGGATC  935
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  AGGAGAAGAAATCTACGTGCTGGTGACGTGGTTAGTTTCAGTAGATCTTAACGGTCAGGATC  900

Qy  936  AACAGTTGTACATTGGGTGGAAGTCGAGATCCGGGTCGAGATTTAGATGCGGGTCGGGTTT  995
         ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db  901  AACAGTTGTACATTGGGTGGAAGTCGAGATCCGAGATCCGGGTCGAGATTTAGATGCGGGTCGGGTTT  960

Qy  996  TGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTAGGAAACA 1055
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Db  961  TGAGATTGTTCGGAGTTAACATTCACCGGAGAGTTCAAGAAACGACGTCGTAGGAAACA 1020

Qy 1056  AAAGAGTGAACGATACTGAGATGTTATCGTTCGTGGTGTGTGAGCAAGAAGCAACGCATCTTTC 1115
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Db 1021  AAAGAGTGAACGATACTGAGATGTTATCGTTCGTGGTGTGTGAGCAAGAAGCAACGCATCTTTC 1080

Qy 1116  ACGGCCTCGTAACAACTCTCTTCTCTTTTTTTTCTTTTGTTGTTGTTCTTTTTAATAATTTTAAAA 1175
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Db 1081  ACGCCTCGTAACGGGCCTTCTCTTCTCTTTTTT--TTGTTGTCTTTTAATAATCTTTAAAA 1140

Qy 1176  ACTCCATTTCGTTTCTTTA-TTTGCATCGGTTCTTTCTTTCTTTGTTTACCAAAGGTTC 1234
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Db 1141  ACTCGCTTTCGTTTCGTTTCTTTCTTTACTTGCATCGGTGTCTTTCTTTGTTTACCAAAGGTTC 1200

Qy 1235  ATGAGTTGTTTTGTGTATT------GATGAACTGTAAATTTTATTTATTACTGAGATAAAT 1287
         |||||||  |||| |||||||      || ||||  ||| || ||||| |||||||||||
Db 1201  CTGAGTTCTTTTTGTGTATTTGCATGCAACTGCTAATATCTTATTTACTGAGATAAAT 1260

Qy 1288  TTTAAAAGGGTTACTTAGAT 1308
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Db 1261  TTTACAAAGGCTTACCTAGAT 1281


RESULT 4
CNS0ABP0
LOCUS       CNS0ABP0      1391 bp    mRNA    linear    HTC  06-FEB-2004
DEFINITION  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
            GSLTPGH37ZC03 of Hormone Treated Callus of strain col-0 of
            Arabidopsis thaliana (thale cress).
ACCESSION   BX816249
VERSION     BX816249.1  GI:42471605
KEYWORDS    HTC; GSLT cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1391)
  AUTHORS   Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
            Temple,G., Caboche.M., Weissenbach,J. and Salanoubat,M.
  TITLE     Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
            A Combined Approach to Evaluate and Improve Arabidopsis Genome
            Annotation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1391)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            Life Technologies (a division of Invitrogen) members carried out
            full-length librairies construction : Temple G.
            Genoscope members carried out sequencing and annotation : Castelli
            V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
            Schachter V., Weissenbach J., Salanoubat M.
            URGV INRA : Clepet C., Caboche M.
            Annotation is based on the June 2003 version of the Arabidopsis
            genome released by MIPS (Munich Information center for Protein
            Sequences). 5 prime and 3 prime are assembled with Phrap.
            http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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ORIGIN

Query Match        88.5%;    Score 1157.6;   DB 3;    Length 1391;
Best Local Similarity  96.9%;   Pred. No. 5.5e-259;
Matches 1246;   Conservative  0;   Mismatches 29;   Indels  11;   Gaps  6;

Qy     34 CACAAACACATTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAACACAGATTAAAT 93
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Db      1 CACAAACACATTCTGTTTTCTCCATTGTTCAAACCATAAAAAAAAACACAGATTAAAT 60

Qy     94 GGAATCGAGTAGCGTTGATGAGAGTACTACAGGTACAAGTTCCATCTGTGAAACCCCGC 153
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Db     61 GGAATCGAGTAGCGTTGATGAGAGTACTACAGGTACAAGTTCCATCTGTGAAACCCCGGC 120

Qy    154 GATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGATCAAG 213
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Db    121 GATAACTCCGGCGAAAAAGTCGTCGGTAGTAACTTATACAGGATGGGAAGCCGGATCAAG 180

Qy    214 CGTTGTGTTAGATTCAGAGAACCGGCTGAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA 273
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Db    181 CGTTGTGTTAGATTCAGAGAACCGGCTGAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAA 240

Qy    274 ATACAAAGGTGTGTGCCACAACCAAACGGAAGATGGGAGCTCAGATTACGAGAAACA 333
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Qy    334 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGT 393
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Db    301 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCGTGCCTACGACGT 360

Qy    394 CGCCGTTCACAGGTTCCGTCGCCGTGACCGCCGTCACAAATTTCAAAGACGTGAAGATGGA 453
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Qy    454 CGAAGACGAGGTCGATTCTGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAG 513
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Qy    514 GAAACATACTTATAACGAGAGAGTTAGAGCAGAGAGATAAACGGCGTCGTAATGGTAACGGAAA 573
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Qy    574 CATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACGGGGTT 633
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Db    541 CATGACTAGGACGTGTTAACGTCGGGGTTGAGTAATGATGGTGTTCTACGACGGGGTT 600

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Qy    694 CCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGT 753
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Db    661 CCGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGT 720

Qy    754 TTCCGTGAAAGGAGTGTTGTTGAACTTGAGGACGTTAACGGAAGTGTGGAGGTTCCG 813
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Qy    934 TCAACAGTTGTACATTGGGTGGGAGTGAAGTCGAGATCCGGGTCAGATTTAGATGCGGGTCGGGT 993
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Qy    994 TTTGAGATTGTTCGGAGTTAACATTTCA-CCGGAGAGTTCAAG-AAACGACGTCGTAGGA 1051
          |||||||||||||||||||||||||| ||      |||||||||| |||||||||||||||||
Db    961 TTTGAGATTTTTCGGAGTTTCACATTTCACATTTCACCCGGAGAGTTCAAGAAACGACGTCGTAGGA 1020

Qy   1052 ----AACAAAGAGTGAACCATACTGAGATGTTA--TCGTTGGTGTGTAGCAAGAAG--C 1103
          |||      || ||||||||||||||||||    |||||||||||||||||||||||
Db   1021 AAACAGAGAGTGAACGATGTAATCGAGATGTTAATCGTTGGTGTGTAGCAAGAAGCAC 1080

Qy   1104 AACGGCATCTTCACGCCTCG-TAACAACTCTTCTTTTTGTTTTTCTTTTGTTTTA 1162
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Db   1081 ACGGCATTCTTCACGCCTCCGTAACACCCCCCTTCTTTTATTTTCTTTTGTATTA 1140

Qy   1163 ATAATTTTAAAAACTCCATTTCGTTTCTTATTGCATCGGTTCTTCTTCTTCTTGTT 1222
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Qy   1223 TACCAAAGGTCATGAGTTGTTTTTGTGTATTGATGAACTGTAAATTTATTTATTAGGA 1282
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Qy   1283 TAAATTTTAAAAAGGGTTACTTAGAT 1308
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Db   1261 TAAATTTTAAAAAGGGTTACTTAGAT 1286


RESULT 5
CNS09Y1T
LOCUS       CNS09Y1T               1387 bp    mRNA       linear   HTC 06-FEB-2004
DEFINITION  Arabidopsis thaliana Full-length cDNA Complete sequence from clone
            GSLTLS56ZA09 of Adult vegetative tissue of strain col-0 of
            Arabidopsis thaliana (thale cress).
ACCESSION   BX841829
VERSION     BX841829.1  GI:42454487
KEYWORDS    HTC; GSLT_cDNA.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 1387)
  AUTHORS   Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
            Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
            Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
  TITLE     Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
            A Combined Approach to Evaluate and Improve Arabidopsis Genome
            Annotation
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1387)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     The sequences are based on single pass reads.
            Life Technologies (a division of Invitrogen) members carried out
            full-length librairies construction : Temple G.
            Genoscope members carried out sequencing and annotation : Castelli
            V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
            Schachter V., Weissenbach J., Salanoubat M.
            URGV INRA : Clepet C., Caboche M.
            Annotation is based on the June 2003 version of the Arabidopsis
            genome released by MIPS (Munich Information center for Protein
            Sequences). 5 prime and 3 prime are assembled with Phrap.
            http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
            _length
            http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
FEATURES             Location/Qualifiers
     source          1..1387
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                     /strain="Col-0"
                     /db_xref="taxon:3702"
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            /clone="GSLTLS56ZA09"
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            /plasmid="pCMVSPORT_6"
    gene    1..1387
            /gene="At1g13260"
ORIGIN

Query Match              84.8%;  Score 1108.6;  DB 3;  Length 1387;
Best Local Similarity    95.2%;  Pred. No. 1.4e-247;
Matches 1176;  Conservative  0;  Mismatches 54;  Indels  5;  Gaps  3;

Qy    1  GTATACATATACACAACACATAATTCACAACACAACACACACATTTCTGTTTTCTCCATT   60
Db  128  GTATACATATACACAACTAATTCACAACACAACACACACATTTCTGTTTTCTCCATT    187

Qy   61  GTTTCAAACCATAAAAAAAAACAGATTAAATGGAATCGAGTAGCGTTGATGAGAGTAC   120
Db  188  GTTTCAGACCATAAGGGGAACACAGATTAAGTGGAATCGAGTAGCGTTGATGAGAGTAC  247

Qy  121  TACAAGTACAGGTTCCATCTGTGAAAC-CCCGGCGATAACTCCGGCGAAAAAGTCGTCGG  179
Db  248  TACAAGTACAGGTTCCATCTGTGAAACGCCCGGCGATAACTCCGGCGAAAGAGTCGTCGG  307

Qy  180  TAGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTTAGATTCAGAGAACGGCG  239
Db  308  TAGGTAACTTATACAGGATGGGAAGCCGGATCAAGCGTTGTGTTTAGATTCAGAGAACGCGG  367

Qy  240  TAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGTGCCACAACCAA  299
Db  368  TAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGTGCCACAACCAA  427

Qy  300  ACGGAAGAGCGGGAGCTCAGATTTACAGAGAAACACCAGCGCGTGGGACATTCA  359
Db  428  ACGGAAGAGATGGGGAGCTCAGATTTACAGAGAAACACCAGCGCGTGGGACATTCA  487

Qy  360  ACGAAGAAGACGAAGCCGCTCGTCGTCCTACGACGTCGCGGTTCCGTCGCCGTG  419
Db  488  ACGAAGAAGACGAAGCCGCTCGTCGTCCTACGACGTCGCGGTTCCGTCGCCGTG  547

Qy  420  ACGCCGTCACAAATTTCAAAGACGTGAAGACGTGAAGACGAAGAGTCGATTTCTTGAATT  479
Db  548  ACGCCGTCACAAATTTCAAAGACGTGAAGACGTGAAGACGAAGAGTCGATTTCTTGAATT  607

Qy  480  CTCATTCGAAATCTGAGATCGTTGATATGTGAGGAAACATACTTATAACGAAGAGTTAG  539
Db  608  CTCATTCGAAATCTGAGATCGTTGATATGTGAGGAAACATACTTATAACGAAGAGTTAG  667

Qy  540  AGCAGAGTAAACGGCGTCGTAATGGTAACGGAAACATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGG  599
Db  668  AGCAGAGTAAACGGCGTCCTAATGGTAACGGAAACATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGG  727

Qy  600  GGTTGAGGTAATGATGGGTTTCTCACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGA  659
Db  728  GGTTGAGGTAATGATGTGGTTTCTCACGACGGGGTTTAGATCGGCGGAGGCACTGTTTGAGA  787

Qy  660  AAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTGGTTATACCGAAACATCACG  719
Db  788  AAGCGGTAACGCGACGCGACGTTGGGAAGCTAAACCGTTGGTTATACCGAAACATCACG  847

Qy  720  CAGAGAAACATTTTCCGTCTCAGTAACCGTCAAGTAACGTTTCCGTGAAAAGGAGTGTGTTGAACT  779
Db  848  CAGAGAAACATTTTCCGTCTCAGTAACCGTCAAGTAACGTTTCCGTGAAAAGGAGTGTGTTGAACT  907

Qy  780  TTGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTTACTCCGTTATTGGAACAGTAGTCAGA  839
Db  908  TTGAGGACGTTAACGGAAAGTGTGGAGGTTCCGTTACTCCGTTATTGGAACAGTAGTCAGA  967

Qy  840  GTTATGTTTTGACTAAAGCTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTGGTG  899
Db  968  GTTATCTCTTGACTAAAGTTGGAGCAGGTTCGTTAAGGAGAAGAATCTACGTGCTGGTG  1027

Qy  900  ACGTGGTTAGTCTCAGTAGATCCTTAACGTCAGGATCAACAGTTGTACATTGGGTGGAAGT  959
Db 1028  ACGTGGTTAGTCTCAGTAGATCCTTAACGTCAGGATCAACAGTTGTACATTGGGTGGAAGT 1087

Qy  960  CGAGATCCGGGTCAGATTTAGATCGCGGTCGGGTTTGAGATTGTTCGAGTTAACATTT 1019
Db 1088  CGAGATCCGGGTCAGATTCAGATCGCGGTCGGGTTTGAGATTGTTCGAGTTAACATTT 1147

Qy 1020  CACCGGAGAGTTCAAGAAACGACGTCGTAGGAACAAAAGAGTGAACGACATACTGAGATGT 1079
Db 1148  CACCGGAGAGTTCAAGAAACGACGTCGTAGGAACAAAACAAAAGAGTGAACGACATACTGAGATGT 1207

Qy 1080  TATCGTT--GGTGTGTAGCAAGAAGCAACGCATCTTCACGCGTCGTAACAACTCTTCTT 1137
Db 1208  TATCGTTCGTAGTGTAGCAAGAAGCAACGCACGCATCTCTCACGCGTCGTAACAACTCTTCTT 1267

Qy 1138  CTTTTTTTTTTGTTGTT--TTAATAATTTTAAAAACTCCATTTTCGTTTTCTT 1195
Db 1268  CTTTTTTTTTTCTTTTGTGTCCCTAATAATTCTTACAAAACTCCCTCCCCCCTCCCCTT 1327

Qy 1196  ATTTGCATCGGTTTCTTTCTCTGTGTTTTACCAAAG 1230
Db 1328  CATCTGCACCGGCTCGTCCCTCTCGTCGTTTACCAAAGG 1362


RESULT 6
BU635864
LOCUS       BU635864                704 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  039F02 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
            sequence.
ACCESSION   BU635864
VERSION     BU635864.1  GI:23303119
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 704)
  AUTHORS   Lundsgaard,M., Emmersen,J., Nielsen,K.L., Wilson,I., Somerville,S.
            and Welinder,K.G.
  TITLE     EST sequencing of Erysiphe cichoracearum infected Arabidopsis
            plants
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Karen G. Welinder
            Institut for bioteknologi
            Aalborg Universitet
            Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
            Tel: +45 96358467
            Fax: +45 98141808
            Email: kgw@bio.auc.dk.
FEATURES             Location/Qualifiers
     source          1..704
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /dev_stage="Plant 3 weeks old, three days post infection"
                     /clone_lib="Infected Arabidopsis Leaf"
                     /note="Organ: Leaf; Vector: pBluescript; Mixed cDNA
                     library of Arabidopsis and B. cichoracearum infected leaf
                     from three weeks old Arabidopsis plants. Plants were
                     harvested 3 days after infection and mRNA oligo dT
                     selected."
ORIGIN

Query Match              51.3%;  Score 670.4;  DB 5;  Length 704;
Best Local Similarity    99.6%;  Pred. No. 1.9e-145;
Matches  693;  Conservative  0;  Mismatches  0;  Indels  2;  Gaps  2;

Qy    1  GTATACATATACACAACACATAATTCACAACACAACACACACATTTCTGTTTTCTCCATT   60
Db   10  GTATACATATACACAACACATAA-TCACAACACAACACACACATTTCTGTTTTCTCCATT   68

Qy   61  GTTTCAAACCATAAAAAAAAACACA-GATTAAATGGAATCGAGTAGCGTTGATGAGAGTA  119
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FEATURES          Location/Qualifiers
     source       1..1048
                  /organism="Brassica napus"
                  /mol_type="mRNA"
                  /cultivar="Westar"
                  /db_xref="taxon:3708"
                  /clone="Bn01b_03b14"
                  /tissue_type="fourth leaf"
                  /dev_stage="3 weeks seedling grown at room temperature"
                  /clone_lib="Bn01b_AAFC_ECORC transgenic Brassica napus_ove
                  rexpressing BNCBF17_constitutively_frost_tolerant"
                  /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
                  Site 2: XhoI; Germinated in soil flats and seedlings grown
                  for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                  light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
                  collected at 9 am and immediately frozen."

ORIGIN

Query Match       46.8%;    Score 612.6;   DB 6;   Length 1048;
Best Local Similarity   81.1%;   Pred. No. 5.7e-132;
Matches   828;   Conservative   4;   Mismatches 153;   Indels 36;   Gaps   9;
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Qy  275 TACAAAGGTGTGTGCCACAACCAAACCGGAAGATGGGAGCTCAGATTTACGAGAAACAC 334
            |||||||  | |  |  ||  | ||||||  |  | |||| |||||| ||||||| |||
Db    1 TACAAAGGCGTCTCCCYTCACCCGAACCGGCGTGGGGAGYTCAGATTYACGAGAAGCAC 60

Qy  335 CAGCGCGTGTGGCTCGGGACATTCAACGAGAAGACAGAAGCGCCGTCGTGCCTACGAGTC 394
            |||||| ||||| ||||| |||||||||||| |||| ||||| ||  || || ||||
Db   61 CAGCGCGTGTGGYTCGGGACTTTCAACGAGAAGACGAGGCGCGCGTTCTTACGACGTG 120

Qy  395 GCGGTTCACAGGTTCCGTCGCCGTGACGCGCCGTCACAAATTCAA-GACGTGAAGATGGA 453
            |||||||| ||||||     | |  |  | ||||| || |||||  | | ||||  |
Db  121 GCGGTTCACCGCKTTCCGAGGCCGAGACCCACGAGCCTCACGAAATTCGGGGCTCGA 180

Qy  454 CGAAGACGAGGTCGATTTCTTGAATTCTCGAATTCTGAATCGAAATCGTTGATATGTTGAG 513
             |||   ||||||     ||||||||    ||||  ||||  ||||| ||||||| ||||
Db  181 CGACGGAGAGGTCGAGTTTTTGAGTTCGGATTCGTTGAATCGTTGATATCTCGAG 240

Qy  514 GAAACATCTTATAACGAAGAGTTAGAGCAGAGAGTAAACGGTCGTCGTAATGGTAACGGAA 573
             |||||| ||||  ||||| ||||||||||||||| | ||||| | ||| |||||| |||
Db  241 GAAGCATACGTATAGCGAAGAGAGCAGAGAGCAGAGCGAAACGGCGAAACGGGTAATGGAA 300

Qy  574 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGCGAGTT 633
             | |||    | ||      ||||  ||  | ||||||||||||  | |  ||| || |
Db  301 CGCGGTTAG----------GTCGACGACGCAAAACGACGGCGTTTCACGACGGCGAGTT 348

Qy  634 TAGATCGGCGGCGAGGCACTGTTTGAAGACGCGTTGGGAGCTGGGAGCGTAACGCGTGGAAGCTAA 693
             ||||| ||||   ||||  ||||| | | | || |||   || ||| ||  ||||||||||||
Db  349 TAGATCGGCGGTCTTGTCTTGTTTGAGAAAAACTGTCACGCCTAGCGACGTTGGGAGCTAA 408

Qy  694 CCGTTGGTTATACCGAAACATCACGCAGAGAAACATTTCGTT---ACCGTCAAGTAA 750
             ||||||||     ||||| | | || || || || ||||||   ||||||||||||
Db  409 CCGTCAGTGATACCGAAACACCACCACGCGGAGAAATATTTTTCCGTTGCCGCGTCGAGTAA 468

Qy  751 CGTTTCCGTGAAAGACGTGTTGTTGAACGTGTTAAGGCGGAAAGTGTGGAGGTT 810
             |||||||||   | | | ||||| |||  || | ||| || |||||| ||||||
Db  469 CGTTTCCGTTTAAGGAGGAGTGTTGTTGAAACTTCGAGACGTGCGCGGGAAAGTGTGGAGGTT 528

Qy  811 CCGTTACTCGTATTGGAACAGTAGTCAGAGTTGTGTTGACTAGGTTGGAACCAGGGTT 870
             ||||||||||||||||||||||| ||||||  ||||| ||||  | |||||| ||||||
Db  529 CCGTTACTCGTATTGGAACAGTAGTCAAAGCTATGTGTTTCTGACAAAAGGTTGGAGCCGGTT 588

Qy  871 CGTTAAGGACGAAGAATCTACGTGCTGGTGACGTGGTAGTTTCAGTAGATCTAACGGTCA 930
             ||||||||  || || |||  | ||| |||||||||| |||| | ||||| |||||||||
Db  589 TGTTAAGGACGAAGAATCTGCCGTCGTGTGATGTGGTTAGTTTGTAGTTTCAGCAGATCCGATGGTCA 648

Qy  931 GGATCAACAGTTGTACATTGGGTGGGAAGTCCGAGATCGGGG-TCAGATTTAGTAGCGGGTC 989
             ||||||| ||| ||| || || ||| ||| || |||||||||  ||||| |||  | ||||
Db  649 GGATCAACAGCTATACATTGGGTGGGAAGTCTAGATCCGGGATCGGGATGTGGAAACGGGTC 708

Qy  990 -GGGTTTGAGATTGTTCGGAGTTAACATTTCACCGGAGAGTTCAAGAAACGACGTCGTA 1048
              ||||||||||||| | ||||| || |  | ||||  ||||  ||||   |||| |||||
Db  709 GGGGTTTGAGACTGTTCGGACTGCTCAACGTTTCACCGGCGGGTTCAAGAAACGACGTCGTA 768
```

```
Db   69 GTTTCAAACCATAAAAARAAAACACAGGATTAAATGGAATCGAGTAGCGTTGATGAGAGTA 128
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Qy  120 CTACAAGTACAGGTTCCATCTGTGAAAACCCGGCGATAACTCCGGCGAAAAAGTCGTCGG 179
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  129 CTACAAGTACAGGTTCCATCTGTGAAAACCCGGCGATAACTCCGGCGAAAAAGTCGTCGG 188
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  180 TAGGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTGTTAGATTCAGAGAACGGCG 239
            ||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||||||
Db  189 TAGGTAACTTATACAGGATGGGAAGCCGATCAAGCGTGTGTTAGATTCAGAGAACGGCG 248
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  240 TAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGCCACAACCAA 299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  249 TAGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGCCACAACCAA 308
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  300 ACGGAAGATGGGAGCTCAGATTTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCA 359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  309 ACGGAAGATGGGAGCTCAGATTTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCA 368
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  360 ACGAAGAAGACGAGAAGCCCGTCGTTGCCTACGACGTCGGGGTTCACAGGTTCCGTCGCCGTG 419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  369 ACGAAGAAGACGAGAAGCCCGTCGTTGCCTACGACGTCGGGGTTCACAGGTTCCGTCGCCGTG 428
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  420 ACGCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGAGTTCTTGAATT 479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  429 ACGCGTCACAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGAGTTCTTGAATT 488
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  480 CTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAGAGAGTTAG 539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  489 CTCATTCGAAATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAGAGAGTTAG 548
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  540 AGCAGAGTAAACGGCTGCGTCGTAATGTAACGAAACATGACTAGGACGTTGTTAACGTCGG 599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  549 AGCAGAGTAAACGGCTGCGTCGTAATGTAACGAAACATGACTAGGACGTTGTTAACGTCGG 608
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  600 GGTTGAGTAATGATGGTGTTTCTACGACGGCGGAGGGCACTGTTTGAGA 659
            ||||||||||||||||||||||||||||||||||||||||||||||||
Db  609 GGTTGAGTAATGATGGTGTTTCTACGACGGCGGAGGGCACTGTTTGAGA 668
            |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  660 AAGCCGTAACGCCAAGCGACGTTGGGAAGCTAAACC 695
            ||||||||||||||||||||||||||||||||||||
Db  669 AAGCCGTAACGCCCAGCGACGTTGGGAAGCTAAACC 704
```

RESULT 7
CB686050

```
LOCUS       CB686050                1048 bp    mRNA    linear   EST 09-APR-2003
DEFINITION  Bn01b_03b14_A Bn01b_AAFC_ECORC transgenic Brassica napus
            overexpressing BNCBF17 constitutively_frost_tolerant Brassica napus
            cDNA clone Bn01b_03b14, mRNA sequence.
ACCESSION   CB686050
VERSION     CB686050.1  GI:29689775
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 1048)
  AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
            Chagnon,J., Farah,S., Couroux,P. and Hattori,J.
  TITLE     Expressed Sequence Tags from constitutively frost tolerant
            transgenic Brassica napus overexpressing BNCBF17
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.gc.ca
```

```
Qy 1049 GGAAACAAAGA--GTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAA 1105
         ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  769 GGGAACAACAGAGTGGTGGTGAACGATACTGAGATGTTATCGTTGGTGTGTGTAGCAAGAAGCAA 828

Qy 1106 CGCATCTCTTCACGGCCTGTAACAACTCCTTCTTCTTTTTTTTCTTTTGTGTTTTAATA 1165
         ||||||||||||||| ||||| |||||||||  ||| ||||||||
Db  829 CGCATCTTTTCACGCCTGTAACCACTCCTCT--------TTCTTGAGTTTTAATA 875

Qy 1166 ATTTTTAAAAACTCCATTTTCGTTTTCTTTATTTGCATCGGTTTCTTCTTCTTGTTTAC 1225
         ||||| |||  ||| ||||| || ||||| ||  ||||||||||||||  |||||| ||
Db  876 ACTTTTTTAATCCACTTCCATTTCTTTTTTTCAGTGCATCAGTTTCTTCTT-AGTAC 934

Qy 1226 CAAAGGTTCATGAGTTGTTTTGTTGTATTGATTGAATGAACTGTAAATTTATTTATAGGATAA 1285
         ||||||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||
Db  935 CAAAGGTTCATGAGTTG-ATTTATTGTAATGATGAACTGTATATCTTATTTATTTATAGGATCA 993

Qy 1286 A 1286
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Db  994 A 994
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RESULT 8
CB257063
LOCUS       CB257063      586 bp    mRNA      linear    EST 06-NOV-2003
DEFINITION  47-E012740-027-002-N12-T7R MPIZ-ADIS-027 Arabidopsis thaliana cDNA
            clone MPIZp772N122Q 5-PRIME, mRNA sequence.
ACCESSION   CB257063
VERSION     CB257063.1  GI:32881836
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 586)
AUTHORS     Schmid,K.J., Soerensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
            Mitchell-Olds,T. and Weisshaar,B.
TITLE       Large-scale identification and analysis of genome-wide
            single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
JOURNAL     Genome Res. 13 (6), 1250-1257 (2003)
MEDLINE     22683290
PUBMED      12799357
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 0049215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 586   Std Error: 0.00
            Plate: 2  row: N  column: 12
            Seq primer: T7R; CTAATACGACTCACTAGGGA.
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                     /ecotype="Ei-2"
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                     /tissue_type="whole plant"
                     /dev_stage="adult plant, mixed stresses"
                     /lab_host="E. coli TOP10"
                     /clone_lib="MPIZ-ADIS-027"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; cDNA
                     library from Arabidopsis thaliana, accession Bifel-2; ten
                     week old total plants grown under long-day conditions in
                     soil, whole adult plants were treated for 24 hours with
                     different stresses, (1) at 4M-0 C in the dark, (2), at 37
                     Grad C in the dark, (3) lying in the lab after removing
                     from soil, (4) in the greenhouse after wounding leaves
                     with a forceps, (5) in the lab watering with a 150 mM
                     NaCl solution, (6) at 26 M-0C in the light/UV; equal
                     quantities of stressed plant material were pooled; library
                     was made at the Max-Planck-Institute for Plant Breeding
                     Research, Cologne, Germany; cloning sites Sali-NotI,
                     primer sites and orientation:
                     T7-SalI-CACGCGTCCG-5prime-cDNA-polyA-CC-NotI-SP6; Note:
                     Sequencing granted in the context of the GABI Arabidopsis
                     Verbund I: Genetic Diversity, 'Establishment of
                     high-efficiency SNP-based mutation detection' PI: Bernd
                     Weisshaar Sequence submission managed by RZPD/GABI-primary
                     database: http://gabi.rzpd.de. This clone is available
                     from RZPD; contact RZPD (clone@rzpd.de) for further
                     information."
```

```
ORIGIN

Query Match             43.3%;   Score 566;  DB 6;  Length 586;
Best Local Similarity   98.8%;   Pred. No. 3.9e-121;
Matches 581;  Conservative  0;  Mismatches  5;  Indels  2;  Gaps  1;

Qy   34 CACAAACACATTTCTGTTTTCTCCATTGTTTCAAACCATAAAAAAAAAACACAGATTAAT 93
         |||||||||||||||||||||||||||||||| ||||| ||||||||  |||||||||| 
Db    1 CACAAACACATTTCTGTTTTCTCCATTGTTTAAACCA--TAAAAAAAACACAGATTAAAT 58

Qy   94 GGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACTACAGGTTCCATCTGTGAAACCCCGGC 153
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   59 GGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACTACAGGTTCCATCTGTGAAACCCCGGC 118

Qy  154 GATAACTCCGGCGAAAAGTCGTCGGTAGTAACTTATACAGGATGGAAGCCGGATCAAG 213
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  119 GATAACTCCGGCGAAAAGTCGTCGGTAGTAACTTATACAGGATGGAAGCCGGATCAAG 178

Qy  214 CGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCGGCTTCCGTCGTCAAA 273
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  179 CGTTGTGTTAGATTCAGAGAACGGCGTAGAAGCGGCTTCCGTCGTCAAA 238

Qy  274 ATACAAAGGTGTGGTGCCACAACCAAACGGAGGATGGGAGCTCAGATTTACGAGAAACA 333
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  239 ATACAAAGGTGTGGTGCCACAACCAAACGGAGGATGGGAGCTCAGATTTACGAGAAACA 298

Qy  334 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGCAGAAGCCGCTCGTCGTCCTACGACGT 393
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  299 CCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGCAGAAGCCGCTCGTCGTCCTACGACGT 358

Qy  394 CGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAGATGGA 453
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  359 CGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCACAAATTTCAAAGACGTGAAGATGGA 418

Qy  454 CGAAGACGAGGTCGATTTCTTGAATTCATTCGAAATCGAGATCGTTGATATGTTGAG 513
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  419 CGAAGACGAGGTCGATTTCTTGAATTCATTCGAAATCGAGATCGTTGATATGTTGAG 478

Qy  514 GAAACATCTTATAACGAAGAGTTAGAGCAGAGAAACGGCGTCGTGTAATGGTAACGGAAA 573
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  479 GAAACATCTTATAACGAAGAGTTAGAGCAGAGAAACGGCGTCGTGTAATGGTAACGGAAA 538

Qy  574 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTC 621
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  539 CATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGGTGTTTC 586
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RESULT 9
AV527557
LOCUS       AV527557      534 bp    mRNA      linear    EST 19-FEB-2004
DEFINITION  AV527557 Arabidopsis thaliana aboveground organs two to six-week
            old Arabidopsis thaliana cDNA clone AP239g12R 5', mRNA sequence.
ACCESSION   AV527557
VERSION     AV527557.1  GI:8867085
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Descurainia sophia cDNA clone Ds01_14g02, mRNA sequence.

ACCESSION   BU238054
VERSION   BU238054.1 GI:22749879
KEYWORDS   EST.
SOURCE   Descurainia sophia
  ORGANISM   Descurainia sophia
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.
REFERENCE   1 (bases 1 to 752)
  AUTHORS   Singh,J.A., Piche,C.L., Couroux,P., De Moors,A., Harris,L.J.,
             Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
  TITLE   Expressed Sequence Tags from Cold-Stressed Descurainia sophia
             Seedlings
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Singh,J.A.
             Eastern Cereal and Oilseed Research Centre
             Agriculture and Agri-food Canada
             KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
             0C6, Canada
             Tel: (613) 759-1662
             Fax: (613) 759-1701
             Email: singhja@agr.gc.ca.
FEATURES   Location/Qualifiers
     source   1..752
                     /organism="Descurainia sophia"
                     /mol_type="mRNA"
                     /db_xref="taxon:89411"
                     /clone="Ds01_14g02"
                     /tissue_type="leaf, stem"
                     /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
                     /clone_lib="Ds01_AAFC_ECORC_cold_stressed_flixweed_seedlin
                     gs"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI;
                     Site_2: Xho I; Plants were grown for 1 month at 20oC/16
                     hrs light/day (average 8 leaves, 1 cm tall, weight
                     0.02g/plant). Then they were exposed to 2oC, 12 hrs
                     light/day, for 1 week. Library prepared by C. Piche using
                     Stratagene kit."
ORIGIN

Query Match   39.6%; Score 518.6; DB 5; Length 752;
Best Local Similarity   81.6%; Pred. No. 4.5e-110;
Matches   621; Conservative   42; Mismatches   81; Indels   17; Gaps   6;

Qy   493 TGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACG 552
          |||||||||||||||||||||||||| :|| :: :||:|::||||||||||||||||||
Db   1 TGAGATCGTTGATATGTTGAGGAAACATACTATACTACWACGWGGWGCTGGAGCAGAGTAAACG 60

Qy   553 GGTCCGTAATGGTAACGGAACATGACTAGGACGTTGTTAACGTGCGGGGTTGAGTAATGA 612
          ||||||||||||||||||||||||||||||||| |||||||||||||||
Db   61 GGTCGTAGCCGGTAACGGAACATGTGAGGACGT------CGTCCGTGTGTTGAATAACGA 114

Qy   613 TGGTGTTTCTACGACGGGGGTTTAGATCGGCGGGAGGCACTGTTTGAGAAAG-CGGTAACGC 671
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   115 CGGGCGGTTGCGACGACGGAGTTTAGATCGGCGGCGGAGCCTCGTTTGAGAAAGYCGGTTACGC 174

Qy   672 CAAGGCGACGTTGGGAAGCTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAACATT 731
          ||||||||||||||||||||||||||||||| |||| ||||||||||||||||||||||
Db   175 CAAGGCGACGTTGGGAAGCTGAACCGTTCGKTTATTCCGAAACACCACCACGCAGAGAAACATT 234

Qy   732 TTCCGTTACCGTCAAGTAACGTTCCGTGAAA-GGAGTGTTGTTGAACTTTGAGACGTT 790
          |||||||||||||||||||||||||||||| ||||||||||| |||||||||||||||
Db   235 TTCCGTTACCGTCAAGTAAATGTTCCGTTAAACGGAGTGCGTGCTGYTGAACYYCGAGGWGCGTG 294

Qy   791 AACGGGAAAGTGTGAGGGTTCCGTTACTCGTATTGAACAGTAGTCAGAGTTATGTTTTG 850
          |||| |||| :||||||||||||||||| :||| :::||||||||::|:|||||: :
Db   295 AACGGAAAAGTGTGAGATTCGGAGATTCGTTATYCGTATYGGAACAGTASYYAAASCCAYGTGTTS 354

Qy   851 ACTAAAAGGTTGGAGCAGCGTTCGTTAAGGAGAGAAAGAAATCTACGTGCTGGTGGTTAGT 910
          |||||||||||||||||||: :||::: :||||| ||||| ::: ||||||||||||||||
Db   355 ACCAAAGGTTGSASCCCSTTCGTTAAGGAGAAGAAAYCTAYGTYGTGTGACGTSGTTAGT 414

RESULT 10
BU238054   BU238054
LOCUS   Ds01_14g02_A Ds01_AAFC_ECORC_cold_stressed_flixweed_seedlings
                                                752 bp   mRNA   linear   EST 06-SEP-2002
DEFINITION Ds01_14g02_A Ds01_AAFC_ECORC_cold_stressed_flixweed_seedlings

---

REFERENCE   1 (bases 1 to 534)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE   A large scale analysis of cDNA in Arabidopsis thaliana: Generation
             of 12,028 non-redundant expressed sequence tags from normalized and
             size-selected cDNA libraries
  JOURNAL   DNA Res. 7 (3), 175-180 (2000)
  MEDLINE   20363093
   PUBMED   10907847
COMMENT   Contact: Erika Asamizu
             The First Laboratory for Plant Gene Research
             Kazusa DNA Research Institute
             Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
             Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES   Location/Qualifiers
     source   1..534
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="AP239g12R"
                     /tissue_type="aboveground organs"
                     /dev_stage="two to six-week old"
                     /clone_lib="Arabidopsis thaliana aboveground organs two to
                     six-week old"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Query Match   40.8%; Score 534; DB 1; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.1e-113;
Matches   534; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   82 CACAGATTAAATGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTG 141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CACAGATTAAATGAATCGAGTAGCGTTGATGAGAGTACTACAAGTACAGGTTCCATCTG 60

Qy   142 TGAAACCCCGGCGATAACTCCGGCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGG 201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TGAAACCCCGGCGATAACTCCGGCGGCGAAAAAGTCGTCGGTAGGTAACTTATACAGGATGGG 120

Qy   202 AAGGCGGATCAAGCGTTGTGTTAGATTCAGAGAACCGCGTGAGAAGCTGAATCTAGGAAGCT 261
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AAGGCGGATCAAGCGTTGTGTTAGATTCAGAGAACCGCGTGAGAAGCTGAATCTAGGAAGCT 180

Qy   262 TCCGTCGTCAAAATACAAAGGTGTGTGCCACAACCCAAACGGAGAGATGGGAGCTCAGAT 321
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCCGTCGTCAAAATACAAAGGTGTGTGCCACAACCCAAACGGAGAGATGGGAGCTCAGAT 240

Qy   322 TTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCG 381
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TTACGAGAAACACCAGCGCGTGTGGCTCGGGACATTCAACGAAGAAGACGAAGCCGCTCG 300

Qy   382 TGCCTACGACGTCGGCGGTTCACAGGTTCCGTCGCGCGGACGCCGTCACAAATTTCAAAGA 441
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TGCCTACGACGTCGGCGGTTCACAGGTTCCGTCGCGCGGACGCCGTCACAAATTTCAAAGA 360

Qy   442 CGTGAAGATGGACGAAGACGAGGTCGATTCTTGAATTCTCATTCCGAAATCTGAGATCGT 501
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CGTGAAGATGGACGAAGACGAGGTCGATTCTTGAATTCTCATTCCGAAATCTGAGATCGT 420

Qy   502 TGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAA 561
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCCGTCGTAA 480

Qy   562 TGGTAACGGAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGG 615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TGGTAACGGAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTAATGATGG 534

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Qy    911 TTCAGTA-GATCTAACGGTCAGGATCAACAGTTGTACATTGGGTGG-AAGTCGAGATCCG  968
          |||||| :|||:.:|||||::|||||||||||||| ||:||||||||| ||||||||||||
Db    415 TTCAGTACGAYCTCMCGSSYCAGSATCAACAGTTCTACMTTGGGTGGCAAGTCGAGATCCG  474

Qy    969 GGTCAGATTTAGATGCGGGTCGGGTTTGAGATTGTTCGGAGTTAACATTCACCGGAGA   1028
          |||| ||.|:|||||||||||||||||||||.|||||||||||:|||||||||||||||
Db    475 GGTCGGACTTGGAAGCGGGTCGGGTTTGAGGTTGTTCGGASTCAACATTCACCGGAGA    534

Qy   1029 GTTCAAGAAAACGACGTCGTAGAAACAAAAGAGTGAACGATACTGAGATGTATCGTTGG   1088
          ||||.|||||||||||||||||.|:||||.|||||||||||||||||||||||||||||
Db    535 GTTCGAGAAAACGACGTCGTAGGGAACAAGAGAGTGAACGATACTGAGATGTATCGTTGG    594

Qy   1089 TGTGTAGCAAGAGCAACGAACCATCTTCACGCCTCGTAACAACTCTTCTTCTTTTTTTTT   1148
          |||||:.:.||||.|||||||||||||.||.|.|||||||||||||||||||||||.|||
Db    595 TGTGTMSTAAGASCAACGAACGTCTTCCACSCCTCGTAACAACTCCTCTTCTCTTTTCTTT    654

Qy   1149 CTTTTGTTGTTTTAATAATTTTTAAAAACTCCATTTTCGTTTTCTTTATTGCATCGGTT   1208
          ||||||.||||||:|::||||||| .||.||||||:|:|||.:||:.|||||||.||||.
Db    655 TTCTTTCTGAATCATTTTTTTT------TCTAATWYCACTDFCGTDDDTWAAATTGTAT    707

Qy   1209 TCTTTCTTCTTCTTCGTTGTTTACCAAAGGTTCATGAGTTGTTTTTGT   1249
          |||| |||.::|:|.||||||||||||||||||||||||||||||||||
Db    708 CGGGTCTTCTDATTTACCAAAGGTTCATGAGTTGTTTTTGT    748
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RESULT 11
AV537025
LOCUS       AV537025                504 bp    mRNA      linear   EST 20-FEB-2004
DEFINITION  AV537025 Arabidopsis thaliana liquid-cultured seedlings Columbia
            Arabidopsis thaliana cDNA clone pAZNII0813R 5', mRNA sequence.
ACCESSION   AV537025
VERSION     AV537025.1  GI:8697308
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 504)
AUTHORS     Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE       A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
JOURNAL     DNA Res. 7 (3), 175-180 (2000)
MEDLINE     20363093
PUBMED      10907847
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1..504
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
                     /clone="pAZNII0813R"
                     /tissue_type="liquid-cultured seedlings"
                     /clone_lib="Arabidopsis thaliana liquid-cultured seedlings
                     Columbia"
                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN

Query Match             38.5%;  Score 504;  DB 1;  Length 504;
Best Local Similarity   100.0%;  Pred. No. 1.1e-106;
Matches  504;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    275 TACAAAGGTGTGTGCCACCAACGAAGAGAGATGGGAGCTCAGATTTACGAGAAACAC    334
          |||||||||||||||||||||||| ||  ||||||||||||||||||||||||||||
Db      1 TACAAAGGTGTGTGCCACCAACCAAACGAAGATGGGAGCTCAGATTTACGAGAAACAC     60
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Qy    335 CAGCGGCGTGTGGCTCGGGACATTCAACGAGAGACGGAGCCGCTCGTGCCTACGACGTC    394
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CAGCGGCGTGTGGCTCGGGACATTCAACGAGAGACGGAGCCGCTCGTGCCTACGACGTC    120

Qy    395 GCGGTTCACAGGTTCCGTCGCCGTGAGCGCCGTCACAAATTCAAAGAGTGAAGATGGAC    454
          |||||||||||||||||||  ||||||||||||||||||||||||||| |||||||||||
Db    121 GCGGTTCACAGGTTCCGTCCGTCGCCGTGAGCGCCGTCACAAATTCAAAGACGTGAAGATGGAC    180

Qy    455 GAAGACAGGAGGTCGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGG    514
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAAGACAGGAGGTCGAATTCTCATTCGAAATCTGAGATCGTTGATATGTTGAGG    240

Qy    515 AAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGTAACGGAAAC    574
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAACATACTTATAACGAAGAGTTAGAGCAGAGTAAACGGCGTCGTAATGTAACGGAAAC    300

Qy    575 ATGACTAGGACGTTGTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTT    634
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ATGACTAGGACGTTGTAACGTCGGGGTTGAGTAATGATGGTGTTTCTACGACGGGGTTT    360

Qy    635 AGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAAC    694
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAAC    420

Qy    695 CGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTT    754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CGTTTGGTTATACCGAAACATCACGCAGAGAAACATTTTCCGTTACCGTCAAGTAACGTT    480

Qy    755 TCCGTGAAAGGAGTGTTGTTGAAC    778
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Db    481 TCCGTGAAAGGAGTGTTGTTGAAC    504
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RESULT 12
AV439943/c
LOCUS       AV439943                546 bp    mRNA      linear   EST 18-FEB-2004
DEFINITION  AV439943 Arabidopsis thaliana above-ground organ two to six-week
            old Arabidopsis thaliana cDNA clone APD29e05_f 3', mRNA sequence.
ACCESSION   AV439943
VERSION     AV439943.1  GI:7610293
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 546)
AUTHORS     Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE       A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
JOURNAL     DNA Res. 7 (3), 175-180 (2000)
MEDLINE     20363093
PUBMED      10907847
COMMENT     Contact: Erika Asamizu
            The First Laboratory for Plant Gene Research
            Kazusa DNA Research Institute
            Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
            Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
FEATURES             Location/Qualifiers
     source          1..546
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /ecotype="Columbia"
                     /db_xref="taxon:3702"
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                     /tissue_type="aboveground organs"
                     /dev_stage="two to six-week old"
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                     /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                     XhoI"
ORIGIN
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Query Match          38.5%;  Score 503.8; DB 1;  Length 546;
Best Local Similarity 97.7%;  Pred. No. 1.2e-106;
Matches 511; Conservative  0; Mismatches  12; Indels  0; Gaps  0;

Qy   778 CTTTGAGGACGTTAACGGGAAAGTGTGGAGGTTCCGTTACTCGTATTGGAACAGTAGTCA 837
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   546 CTTTGAGTACGTTAACCGAAAAGTGTGAAGGTTCCGTTACTCGTATTGGAACAGTAGTCA 487

Qy   838 GAGTTATGTTTGACTAAGGTTGGAGCAGGTTCGTTAAGGAGGAAGAATCTACGTGCTGG 897
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 GAGTTATGTTTGACTAAGGTTGGAGCAGGTTCGTTAAGGAGGAAGAATCTACGTGCTGG 427

Qy   898 TGACGTGGTTAGTTTCAGTAGATCTAACGGTCCAGGATCAACAGTTGTACATTGGGTGAA 957
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Db   426 TAACGTGGTTAGTTTCAGTAGATGTAACCGTCAGGATCAACAGTTGTACATTGGGTGAA 367

Qy   958 GTCGAGATCCGGGTCAGATTTAGATGCGGGGTCCGGGTTTGAGATTGTTCGGAGTTAACAT 1017
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366 GTCGAGATCCGGGTCAGATTTAGATGCGGGTCCGGGTTTGAGATTGTTCGGAGTTAACAT 307

Qy  1018 TTCACCGGAGAGTTCAAGAAACGACGTCCTAGGAAACAAAAGAGTGAACGATACTGAGAT 1077
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   306 TTCACCGGAGAGTTCAAGAAGCGACGTCCTAGGAAACAAAAGAGTGAACGATACTGAGAT 247

Qy  1078 GTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTT 1137
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   246 GTTATCGTTGGTGTGTAGCAAGAAGCAACGCATCTTTCACGCCTCGTAACAACTCTTCTT 187

Qy  1138 CTTTTTTTTTTCTTTTGTTTTGTTTGTTTTAATAATTTTAAAAACTTCGTTTTTCTTTAT 1197
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   186 CTTGTTTTTTTCTTTTGTTTTGTTTGTTTTAATAAGTTTTAAAAACTTCCATGTTCGTTTTTCTTTAT 127

Qy  1198 TTGCATCGGTTTCTTCTTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTTGTGTATTGA 1257
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   126 ATGCATCGGTTTCTTCTTTCTTGTTTACCAAAGGTTCATGAGTTGTTTTTGTTGTATTGA 67

Qy  1258 TGAACTGTAAATTTTATTTATAGGATAAAATTTTAAAAAAGGGTT 1300
         ||||||||||||||||||||||||||||||||||||||
Db    66 TGAACTGTAAATTTTATTTATAGGATAAAATTTTAAAAAGGGAT 24

RESULT 13
BZ458719/c
LOCUS       BZ458719         969 bp    DNA       linear    GSS 13-DEC-2002
DEFINITION  BONKU85TF BO_1.6_2_KB tot Brassica oleracea genomic clone BONKU85,
            genomic survey sequence.
ACCESSION   BZ458719
VERSION     BZ458719.1  GI:2673945
KEYWORDS    GSS.
SOURCE      Brassica oleracea
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 969)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other GSSs: BONKU85TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1..969
                     /organism="Brassica oleracea"
                     /mol_type="genomic DNA"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BONKU85"
                     /clone_lib="BO_1.6_2_KB tot"
                     /note="Vector: pHOS1; Site 1: BstXI; 1.6-2 kb sheared
                     total DNA inserted into pHOS1 using BstXI linkers"
ORIGIN

Query Match          37.8%;  Score 493.8; DB 8;  Length 969;
Best Local Similarity 76.6%;  Pred. No. 2.8e-104;
Matches 684; Conservative  0; Mismatches 169; Indels 40; Gaps  5;

Qy   127 TACAGGTTCCATCTGTGAAACCCGGCGATAACTCCGGCGAAAAAGTCGTCGGTAGGTAA 186
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Db   879 TCCACTCCGGTCAAGATACACCGCCCGAGACGGCGGAAGTCGTCATCTCCGGCGAG 820

Qy   187 CTTATACAGGATGGGAAGCGGGATCAAGCGGTTGTGTTTGAGATTCAGAGACGGCGTAGAGC 246
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   819 TTTATACAGAAATGGGAAGCGGCGGTTCAAGCGTGGTTCTCGAATTCCCAGAACGGCGTCGAAGC 760

Qy   247 TGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAACGAAG 306
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   759 AGAATCAAGAAAGCTCCCGTCGTCAAATTCAAAGGCGTCGTCCTCAGCCAAACGGAAG 700

Qy   307 ATGGGGAGCTCAGATTTACGAGAAACACCAGCGCGTGTGCTCGGACATTCAACGAAGA 366
         ||||||||||||||||||||||||||||||||||||||||||||||
Db   699 ATGGGGAGCTCAGATATACGAGAAGCACAAGGCGGTTTGCTCGGGACATTCAACGAAGA 640

Qy   367 AGACGAAGCCGCTCGTGCCTACGACGTCCGCGGTTCACAGGTTCGTCGCCTGACGCGCCGT 426
         ||||||||||||||||||||||||||||||||
Db   639 AGAGAAGCGGCGCGTGTCTACGACGTGCCGCTCACCGGTTTCCGCGGCTCTGACGCGCCGT 580

Qy   427 CACAAATTTCAAAGACGTGAAGATG----------GACGAAGACGAGGTCGA 468
         ||                         ||||||||||||||
Db   579 CACTAAATTTCAAACCAGACACGACGTTCCCTAACCGTGAAGGTGACGGAGCAGGAAGTAAA 520

Qy   469 TTTCTTGAATTCTCATTCGAAATCTGAGATCGTTGATAATGTTGAGGAAACATACTTATAA 528
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   519 GTTCTTAAACGCACCACATTCGAAATATGAAATATGTTGATATGTTGAGGAAACACACTTACAA 460

Qy   529 CGAAGAGTTAGAGCAGCAGAGTAAACGGCTCGTAA---TGGTAACGAAGAACATGACTAGGAC 585
         |||||||||||||||||||||||||||||||||||                |||||
Db   459 AGAAGAGTTAGAGCAGCAGAGAACGCAAACGTAACGGTGTGTAACACGGAAGAAGAGAC 400

Qy   586 GTTGTTAACGTCGGGGTTGAGTAATGATGTGTTTCTACGACGGGGTTTAGATCGGCGGA 645
         |||                             ||||||||||||||
Db   399 GGCGTT---------TGCTAACGTTACGGTTGTGACGGCGGTTTAAAACCGGGCGGA 355

Qy   646 GGCACTGTTTGAGAAAGCGGTAACGCCAAGCGACGTTGGGAAGCTAAACCGTTTCGTTAT 705
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   354 GTGTCTGTTTGAGAAAACGGTAACGCCGAGTGACGTGCGGGAGCTAAACCGTTTAGTGAT 295

Qy   706 ACCGAAACATCACGCAGAGAAACATTTCCGTCAA---GTAACGTTCCGTGAA 762
         |||||||||||||||||||||||||||||||||                ||||||||
Db   294 ACCGAAACACCAAGCCGAGAAACATTTTCCGTTAACCGGCGACGTCTCCGTGAG 235

Qy   763 AGGAGTGTGTTGAACTTTGGACGTTGGAGGTGGAAAGTGTGGAGGTTCCGTTACTCGTA 822
         ||||  |||||                     ||||||||||||||
Db   234 AGGGACGCTGTTGAATTTCGAAGACGTGAATTTTAAAAGATCTAACGGTTCAGGATCAACAGTT 175

Qy   823 TTGGAACAGTAGTCAGTAGGAAGT-CGAGATCCGGGTCGATTTAGATGCGGGTCGGGTT 882
         |||||||||||||||||||||||||                        |||||
Db   174 TTGGAACAGTAGTCAGTCAAAGCTCACGTGTTGACTAAAGGTTGGAGCAGGTTCGTTAAAGAGAA 115

Qy   883 GAATCTACGTGCTGGTGACGTGGTTAGTTCAGTAGATCTAACGGTCAACAGTT 942
         ||||  |||                         ||||||||||
Db   114 GAGACTCTGTGCCGGTGATCAGTTTTAAAAGATCTAACGGTCAGGATCAACAGTT 55

Qy   943 GTACATTGGGTGGAAGT-CGAGATCCGGGTCGGTTCAGATTTAGATGCGGGTCGGGTT 994
         ||||||||||||                       ||||||
Db    54 GTATATTGTGTGGAAGTACAAAGGCTGGGTTGGAACAGGATACGGGCGCGGGTT 2
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RESULT 14
AJ597800
LOCUS   AJ597800   860 bp   DNA   linear   GSS 15-JAN-2004
DEFINITION   Arabidopsis thaliana T-DNA flanking sequence, left border, clone
             457A08, genomic survey sequence.
ACCESSION   AJ597800
VERSION   AJ597800.1 GI:37947428
KEYWORDS   GSS; left border; T-DNA flanking sequence.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
             Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
             Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE   T-DNA integration into the Arabidopsis genome depends on sequences
             of pre-insertion sites
JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE   22363535
PUBMED   12446565
REFERENCE   2 (bases 1 to 860)
AUTHORS   Balzergue,S.
TITLE   Direct Submission
JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
             Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT   PCR was performed on DNA from transformants of Arabidopsis thaliana
             plants from INRA (Versailles). The DNA fragment(s) resulting from
             the PCR were directly sequenced from the left or the right border
             to determine the genomic sequence flanking the insertion. T-DNA
             derived sequences were removed. Information to order the
             corresponding mutant line and a link to a database providing a
             graphical display of the insertion site are available at
             http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
             been generated in the framework of the French plant genomics
             program 'Genoplante' (http://www.genoplante.com and
             http://genoplante-info.infobiogen.fr).
FEATURES   Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /cultivar="Wassilewskija"
                     /db_xref="taxon:3702"
                     /clone="457A08"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature   1..860
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

Query Match   37.7%; Score 493.4; DB 9; Length 860;
Best Local Similarity 91.2%; Pred. No. 3.4e-104;
Matches   557; Conservative   0; Mismatches 51; Indels   3; Gaps   3;

Qy   1 GTATACATATACACAACATAATTCACACAACACAACAACAACATTCTGTTTTCTCCATT 60
          ||||||||||||||||||||||| ||||||||||||||||||||||||||| ||||||||
Db   253 GTATACATATACACAACACTAATTCACACAACACAACAACAACATTCTGTTTTCTCCATT 312

Qy   61 GTTTCAAACCATAAAAAAAAACACAGATTAAATGGAATGCAGGCGTTGATGAGAGTAC 120
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   313 GTTTCAAAGCAT-AAAAAAAACACAGATTAAATGGAATGCAGGCGTTGATGAGAGTAC 371

Qy   121 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   372 TACAAGTACAGGTTCCATCTGTGAAACCCCGGCGATAACTCCGGCGAAAAAGTCGTCGGT 431

Qy   181 AGGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTTAGATTCAGAGAACGCGCGT 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   432 AGGTAACTTATACAGGATGGGAAGCGGATCAAGCGTTGTTGTTAGATTCAGAGAACGCGCGT 491

Qy   241 AGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   309 GGGGAGCTCAGATTTACGAGAAACACCAGCGCCGGTCGTGGTGCCACAACCAAA 368

492 AGAAGCTGAATCTAGGAAGCTTCCGTCGTCAAAATACAAAGGTGTGGTGCCACAACCAAA 551
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 CGGAAGATGGGGAGCTCAGATTTACGAGAAACACCAGCGCCGTCGTGGCTCGGACATTCAA 360

552 CGGAAGATGGGGAGCTCAAATTTACGAGAAACACCAGCGCCGTCGTGGCTCGGACATTCAA 611
    ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
361 CGAAGAGACGAAGCCGCTCGTCGTCCTACGACGTTCGCGACGTTCCGTCGTCGCCGTGA 420

361 CGAAGAGACGAAGCCGCTCGTCGTCCTACGACGTTCGCGACGTTCCGTCGTCGCCGTGA 420
    |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
612 CGAAGAGACGAAGCCGCTCGTCGTCCTACGACGTTCGCGACGTTCCAAGTTCCGTCGCCGTGA 671

421 CGCCGTCACAAATTCAAAGACGTGAAGACGTGACGAGAGGTCGATTTCTTGAATTC 480
    ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
672 CGCCGGCACAAATTTCAAGACGTGAAAATGGGAACGAGAGCGAGGTCAATTTCTTGAATTC 731

481 TCATTCGAAATCTGAGATCGTTGTTGATATGTTGACGGAAACATACTTATAACGAAGAGTTAGA 540
    |||| ||||||||||||||||||||||| |||||||||||||||||||||||||||||||
732 TTATTCGGAAATTGAAATCGTGGAAATATGTGAGAAACTTCTTTATAAC-AAAAGTTAGA 790

541 GCAGAGTAAACGGCGTCGTAATGGTAACGGACGAAACATGACTAGGACGTGTTAACGTCGGG 600
    ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
791 GCA-AATAAACCGCGCGGCCGTAATGGTACCGGACGACTAAGACCTTTAAACGCCGGG 849

601 GTTGAGTAATG 611
    ||||| |||||
850 GTTGAATAATG 860

RESULT 15
AI994740
LOCUS   AI994740   480 bp   mRNA   linear   EST 08-SEP-1999
DEFINITION   701499474 A. thaliana, Ohio State clone set Arabidopsis thaliana
             cDNA clone 701499474, mRNA sequence.
ACCESSION   AI994740
VERSION   AI994740.1 GI:5841645
KEYWORDS   EST.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 480)
AUTHORS   Chen,J., Momiyama,M., Chan,E., Mooney,M., Carroon,B., Gilliland,D.,
             Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P.,
             Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D.,
             Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C.,
             Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S.,
             Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and
             Hanson,D.
TITLE   Arabidopsis thaliana Gene Expression MicroArray
JOURNAL   Unpublished (1999)
COMMENT   Contact: David Smoller, Ph.D.
             Genome Systems, Inc., a wholly owned subsidiary of Incyte
             Pharmaceuticals, Inc.
             4633 World Parkway Circle, St. Louis, MO 63134, USA
             Tel: 877-577-2733
             Fax: 314-427-3324
             Email: service@genomesystems.com.
FEATURES   Location/Qualifiers
     source   1..480
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /clone="701499474"
                     /clone_lib="A. thaliana, Ohio State clone set"
                     /note="cDNA library was made from selected clones from the
                     Arabidopsis thaliana Ohio State clone set."
ORIGIN

Query Match   36.6%; Score 478.4; DB 1; Length 480;
Best Local Similarity 99.8%; Pred. No. 1e-100;
Matches   479; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   309 GGGGAGCTCAGATTTACGAGAAACACCAGCGCCGGTCGTGGTGCCACAACCAAA 368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||

Tue Sep 13 10:10:52 2005

Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        1 GGGGAGCTCAGATTTACGAGAAACACCAGCGCCGTGTGCTCGGGACATTCAACGAAGAAG 60

Qy   369 ACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCA 428
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ACGAAGCCGCTCGTGCCTACGACGTCGCGGTTCACAGGTTCCGTCGCCGTGACGCCGTCA 120

Qy   429 CAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGA 488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CAAATTTCAAAGACGTGAAGATGGACGAAGACGAGGTCGATTTCTTGAATTCTCATTCGA 180

Qy   489 AATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTA 548
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AATCTGAGATCGTTGATATGTTGAGGAAACATACTTATAACGAAGAGTTAGAGCAGAGTA 240

Qy   549 AACGGCGTCGTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTA 608
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AACGGCGTCGTAATGGTAACGGAAACATGACTAGGACGTTGTTAACGTCGGGGTTGAGTA 300

Qy   609 ATGATGGTGTTTCTACGACGGGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAA 668
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATGATGGTGTTTCTACGACGGGGTTAGATCGGCGGAGGCACTGTTTGAGAAAGCGGTAA 360

Qy   669 CGCCAAGCGACGTTGGGAAGCTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAAC 728
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CGCCAAGCGACGTTGGGAAGCTAAACCGTTGGTTATACCGAAACATCACGCAGAGAAAC 420

Qy   729 ATTTTCCGTACCGTCAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGACG 788
           |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   421 ATTTTCCGTTACCGTCAGTAACGTTTCCGTGAAAGGAGTGTTGTTGAACTTTGAGGGCG 480

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Job time : 5003.21 secs

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